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OM protein - protein search, using SW model

Run on: February 14, 2005, 15:01:02 ; Search time 177 Seconds

Perfect score: 3406 (without alignment(s))

Sequence: 1 MNPNNRSEHDTIKVTPNSEL,.....SFVSNBKIYTDKIEFIPVQL 652

1886.303 Million cell updates/sec

Title: US-10-614-076-98

Scoring table: BL0SUM62 Gapext 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	3406	100.0	652	1	C3BB_BACTU	006117 bacillus th	
2	3212	94.3	659	1	C3BA_BACTU	P11969 bacillus th	
3	2341.5	68.7	644	1	C3AA_BACTU	P01130 bacillus th	
4	2341.5	68.7	652	2	09S6N9	09S6N9 bacillus th	
5	2337.5	68.6	652	2	06PNX8	06PNX8 bacillus th	
6	2319.5	68.1	652	2	Q643Z7	Q643Z7 bacillus th	
7	2132	63.2	649	1	C3CA_BACTU	Q45744 bacillus th	
8	1272	37.4	1144	2	Q8KL7	Q8KL7 bacillus th	
9	1205.5	35.4	1157	1	CBAA_BACUR	Q45104 bacillus th	
10	1166.5	34.2	1169	1	C8BA_BACUR	Q45705 bacillus th	
11	1127	33.1	1157	1	C9CA_BACTU	Q45733 bacillus th	
12	1124	33.0	719	1	C1IB_BACTU	Q4509 bacillus th	
13	1122	32.9	1229	1	C1BB_BACTU	Q45739 bacillus th	
14	1122	32.9	1233	1	C1CB_BACTU	Q45774 bacillus th	
15	1121	32.9	1215	1	C1KA_BACTU	Q4515 bacillus th	
16	1119	32.3	1138	1	C7AA_BACTU	Q03749 bacillus th	
17	1118.5	32.3	719	2	Q9F058	Q9F058 bacillus th	
18	1117	32.8	1138	1	C7AB_BACUR	Q4508 bacillus th	
19	1115.5	32.8	719	1	C1ID_BACTU	Q4501 bacillus th	
20	1112	32.6	1138	1	C7AB_BACTU	Q4572 bacillus th	
21	1100.5	32.3	719	1	C1IA_BACTU	Q4515 bacillus th	
22	1100.5	32.3	719	2	Q93N95	Q93N95 bacillus th	
23	1100.5	32.3	719	2	Q6X181	Q6X181 bacillus th	
24	1096.5	32.2	719	2	Q8K761	Q8K761 bacillus th	
25	1094.5	32.1	719	2	Q85796	Q85796 bacillus th	
26	1072.5	31.5	1228	1	C1BA_BACTU	P0515 bacillus th	
27	1071.5	31.5	1228	2	Q93N95	Q93N95 bacillus th	
28	1070.5	31.4	1228	2	Q93T75	Q93T75 bacillus th	
29	1060	31.1	1160	1	C8CA_BACTP	Q45706 bacillus th	
30	1060	31.1	1160	2	Q6RR6	Q6RR6 bacillus th	
31	1053	30.9	1231	2	Q8KNY2	Q8KNY2 bacillus th	

32	1046.5	30.7	719	1	C1IC_BACTU	087404 bacillus th
33	1042	30.6	1231	1	C1BD_BACTU	092425 bacillus th
34	1041.5	30.6	1169	1	C9DA_BACTP	006014 bacillus th
35	1018	29.9	1154	2	Q6QAN9	Q6QAN9 bacillus th
36	1013	29.7	849	2	Q6PYW8	Q6PYW8 bacillus th
37	1013	29.7	1227	1	C1BE_BACTU	Q98503 bacillus th
38	999.5	29.3	645	2	Q9S6D3	Q9S6D3 bacillus th
39	995	29.2	1150	1	C9EA_BACTA	Q9zn19 bacillus th
40	995	29.2	1150	2	Q71RE4	Q71RE4 bacillus th
41	975	28.6	1163	1	CQAA_BACTF	Q9x537 bacillus th
42	963.5	28.3	1144	2	Q45745	Q45745 bacillus th
43	934.5	27.4	1189	1	C1CA_BACTE	P05518 bacillus th
44	934.5	27.4	1189	2	Q6IN8B	Q6ynb8 bacillus th
45	932.5	27.4	1189	2	Q9LB77	Q9LB77 bacillus th
46	909	26.7	793	2	Q6PYW7	Q6PYW7 bacillus th
47	899.5	26.4	1155	1	C1AB_BACTK	P06578 bacillus th
48	899.5	26.4	1155	2	Q7BEB8	Q7BEB8 bacillus th
49	899.5	26.4	1155	2	Q9E296	Q9E296 bacillus th
50	898.5	26.4	1156	2	Q6GUA7	Q6Gua7 bacillus th
51	898.5	26.4	1174	1	C1FA_BACTA	Q3744 bacillus th
52	897	26.3	1118	2	Q9Am83	Q9Am83 bacillus th
53	893.5	26.2	1177	2	Q6EIX3	Q6eix3 bacillus th
54	891.5	26.2	1155	1	C1AE_BACTL	Q93T21 bacillus th
55	888	26.1	1181	1	C1CB_BACTG	P56553 bacillus th
56	886.5	26.0	1176	1	C1AD_BACTA	Q3744 bacillus th
57	883.5	25.9	1179	2	Q7WT9	Q7wt9 bacillus th
58	876	25.7	1176	2	Q9S5V8	Q9S5V8 bacillus th
59	874	25.7	1180	2	Q9SSV8	Q9SSV8 bacillus th
60	873.5	25.6	1171	2	Q66894	Q66894 bacillus th
61	870	25.5	620	2	Q45720	Q45720 bacillus th
62	870	25.5	1176	2	Q45736	Q45736 bacillus th
63	869.5	25.5	1171	1	C1EA_BACTX	Q71bw6 bacillus th
64	869.5	25.5	1171	2	Q45735	Q45735 bacillus th
65	867.5	25.5	1177	2	Q8GLT5	Q8GLT5 bacillus th
66	867.5	25.5	1177	2	Q8G9Y5	Q8g9y5 bacillus th
67	867	25.5	1178	1	C1AC_BACTK	P05068 bacillus th
68	867	25.5	1178	2	Q6XLN7	Q6xln7 bacillus th
69	866.5	25.4	1166	1	C1GA_BACTU	Q45746 bacillus th
70	866	25.4	1176	1	C1AA_BACTK	P02965 bacillus th
71	865.5	25.4	829	2	Q6B8D6	Q6be06 bacillus th
72	865	25.4	1176	2	Q9RC30	Q9rc30 bacillus th
73	863	25.3	1178	2	Q9R826	Q9r826 bacillus th
74	862	25.3	618	2	Q32306	Q32306 bacillus th
75	861.5	25.3	607	2	Q45721	Q45721 bacillus th
76	861.5	25.3	618	2	Q45737	Q45737 bacillus th
77	861.5	25.3	723	2	Q9S8B5	Q9s8b5 bacillus th
78	861.5	25.3	1177	2	Q31743	Q31743 bacillus th
79	861.5	25.3	1177	2	Q71JF1	Q71Jf1 bacillus th
80	861	25.3	1178	2	Q45768	Q45768 bacillus th
81	859.5	25.2	1170	1	C1JB_BACTU	Q45716 bacillus th
82	854.5	25.1	1169	1	C1DA_BACTA	Q8q1eb bacillus th
83	850.5	25.0	1169	1	C1GB_BACTZ	Q9raZ6 bacillus th
84	846	24.8	1169	1	C1FB_BACTM	Q66377 bacillus th
85	845	24.8	1169	1	C1DB_BACTU	Q45749 bacillus th
86	844	24.8	1167	1	C1JA_BACTU	Q45738 bacillus th
87	841	24.7	648	2	Q6BB09	Q6bb09 bacillus th
88	838.5	24.6	1165	1	C1DA_BACTA	P19a15 bacillus th
89	838	24.6	793	2	Q6PYW9	Q6pyw9 bacillus th
90	835	24.5	1174	1	C1BB_BACTA	Q3745 bacillus th
91	828	24.3	1160	1	C1DB_BACTU	Q45749 bacillus th
92	828	24.3	1160	2	Q93TF9	Q93tf9 paenibacill
93	821	24.1	1332	2	Q6GPW6	Q6gpw6 bacillus th
94	816	24.0	1332	2	Q763X5	Q763x5 bacillus th
95	811.5	23.8	660	2	Q8RQW6	Q8rqw6 bacillus th
96	810.5	23.8	1118	2	Q9AM82	Q9am82 bacillus th
97	807	23.7	1176	2	Q9SS14	Q9ss14 bacillus th
98	805.5	23.6	1344	2	Q765X7	Q765x7 paenibacill
99	797.5	23.4	782	2	Q6PWT6	Q6pwt6 bacillus th
100	796	23.4	911	1	C1AF_BACTU	P93115 bacillus th
101	788	23.1	1155	1	C1HB_BACTM	Q45718 bacillus th
102	787.5	23.1	1172	1	C1HA_BACTU	Q45748 bacillus th
103	783	23.0	1176	1	C1AG_BACTU	Q98515 bacillus th
104	773.5	22.7	686	2	Q75Q5	Q75q5 bacillus th

105	748.5	22.0	1118	2	Q9AMB81	O9amb1	bacillus	th	06Q706	bacillus	th	RL	Appl. Environ. Microbiol.	58:3921-3927(1992).
106	745	21.9	1170	2	Q8QTC6	Q6g706	bacillus	th	08Q707	bacillus	th	RN	[2]	SEQUENCE FROM N.A.
107	718	21.1	682	1	CIBA_BACTU	Q4570	bacillus	th	04570	bacillus	th	RP	SEQUENCE FROM N.A.	STRAIN=NRRL B-18655 / EG5144;
108	700	20.6	381	2	Q45740	Q8vdk9	bacillus	th	08vdk9	bacillus	th	RC	SEQUENCE FROM N.A.	RA Donovan W.P., Rupar M.J., Slaney A.C.; protein toxic to coleopteran
109	685	20.1	1280	2	Q8VUK9	Q99031	bacillus	th	Q99031	bacillus	th	RA	"Bacillus thuringiensis cryIIIC, (b) protein toxic to coleopteran	RT insects.
110	679	19.9	1156	1	C3AA_BACTG	Q76533	paeinbacill	th	Q76533	paeinbacill	th	RT	RT insects.	PATENT NUMBER US578625, 03-JAN-1995.
111	676.5	19.9	405	2	Q765X3	Q8kra2	bacillus	th	Q8kra2	bacillus	th	RL	PATENT NUMBER US578625, 03-JAN-1995.	-1- FUNCTION: Promotes collodiosmotic lysis by binding to the midgut epithelial cells of Coleoptera. Has moderate level of toxicity to southern corn rootworm.
112	669.5	19.7	675	2	Q8KNAV2	P09652	bacillus	th	P09652	bacillus	th	CC	-1- FUNCTION: Promotes collodiosmotic lysis by binding to the midgut epithelial cells of Coleoptera. Has moderate level of toxicity to southern corn rootworm.	CC
113	663.5	19.5	1236	2	Q919T3	Q93933	bacillus	th	Q93933	bacillus	th	CC	CC	CC
114	663.5	19.5	1236	1	CIBA_BACTI	P05519	bacillus	th	P05519	bacillus	th	CC	CC	CC
115	656.5	19.3	1136	1	CIBA_BACTI	Q6be03	bacillus	th	Q6be03	bacillus	th	CC	CC	CC
116	639	18.8	810	2	Q6BE03	P1640	bacillus	th	P1640	bacillus	th	CC	CC	CC
117	639	18.7	1180	1	CIBA_BACTI	Q6bc05	bacillus	th	Q6bc05	bacillus	th	CC	CC	CC
118	631.5	18.5	675	2	Q8CBH5	Q9x662	bacillus	th	Q9x662	bacillus	th	CC	CC	CC
119	626.5	18.4	1109	1	C3AA_BACTI	Q87905	bacillus	th	Q87905	bacillus	th	CC	CC	CC
120	625	18.4	674	1	CORA_BACTU	Q9fd50	bacillus	th	Q9fd50	bacillus	th	CC	CC	CC
121	623.5	18.3	1128	2	Q9FDG0	Q8vul0	bacillus	th	Q8vul0	bacillus	th	CC	CC	CC
122	613	18.0	1254	2	Q8VUL0	Q8vw62	bacillus	th	Q8vw62	bacillus	th	CC	CC	CC
123	604	17.7	666	2	Q8WV62	Q7x3F7	bacillus	th	Q7x3F7	bacillus	th	CC	CC	CC
124	600.5	17.6	666	2	Q7X3F7	Q3221	bacillus	th	Q3221	bacillus	th	CC	CC	CC
125	600	17.6	753	1	CIBA_BACUF	Q75va2	bacillus	th	Q75va2	bacillus	th	CC	CC	CC
126	594.5	17.5	683	2	Q75VA2	Q8vnx2	bacillus	th	Q8vnx2	bacillus	th	CC	CC	CC
127	573.5	16.8	650	2	Q8VNX2	Q8vnx1	bacillus	th	Q8vnx1	bacillus	th	CC	CC	CC
128	573.5	16.8	688	2	Q8VNX1	Q87906	bacillus	th	Q87906	bacillus	th	CC	CC	CC
129	535	15.7	675	1	CIBA_BACTJ	Q9s597	bacillus	th	Q9s597	bacillus	th	CC	CC	CC
130	534	15.7	826	1	CIBA_BACUH	Q95102	clostridium	th	Q95102	clostridium	th	CC	CC	CC
131	520	15.3	618	1	CIBA_CLOBI	Q9AMB80	bacillus	th	Q9AMB80	bacillus	th	DR	EMBL	M89794; AAA22334_1; -
132	483	14.2	1155	2	Q9AMB80	Q75va1	bacillus	th	Q75va1	bacillus	th	DR	EMBL	U31633; AAA74198_1; -
133	482	14.2	613	1	CGNA_CLOBI	Q8vnx1	bacillus	th	Q8vnx1	bacillus	th	DR	PIR	I39811; I39811;
134	472	13.9	1270	2	Q8VUL1	Q45789	bacillus	th	Q45789	bacillus	th	DR	PDB	I1116; X-ray; A=64-652.
135	316	9.3	1257	1	C3CA_BACTU	Q45789	bacillus	th	Q45789	bacillus	th	DR	InterPro	IPI00178; Endotoxin C.
136	301	8.8	297	2	Q45789	Q45789	bacillus	th	Q45789	bacillus	th	DR	InterPro	IPI005639; endotoxin N.
137	279.5	8.2	1245	1	C5BA_BACTU	Q8kz02	bacillus	th	Q8kz02	bacillus	th	DR	InterPro	IPI005639; endotoxin N.
138	277.5	8.1	1286	2	Q8KZM2	P056956	bacillus	th	P056956	bacillus	th	DR	InterPro	IPI008979; Gal_bind_Like.
139	272.5	8.0	1167	1	CIBA_BACTU	Q9rmq3	bacillus	th	Q9rmq3	bacillus	th	DR	Pfam	PF03944; Endotoxin C; 1.
140	262	7.7	633	1	C2AD_BACTU	Q6s554	bacillus	th	Q6s554	bacillus	th	DR	Pfam	PF00555; Endotoxin M; 1.
141	255.5	7.5	196	2	Q6s554	Q6kf60	bacillus	th	Q6kf60	bacillus	th	DR	Pfam	PF03945; Endotoxin N; 1.
142	251.5	7.4	633	2	Q6KF60	Q9s6n5	bacillus	th	Q9s6n5	bacillus	th	KW	3D-structure; sporulation; toxin.	
143	248.5	7.3	633	2	Q9s6n5	Q6s553	bacillus	th	Q6s553	bacillus	th	FT	VARIANT	21 Q -> P (in strain EG5144).
144	247.5	7.3	193	2	Q6s553	Q8gh90	bacillus	th	Q8gh90	bacillus	th	FT	VARIANT	97 N -> D (in strain EG5144).
145	247	7.3	633	2	Q8GH90	P21253	bacillus	th	P21253	bacillus	th	FT	VARIANT	289 I -> V (in strain EG5144).
146	245.5	7.2	633	1	C2AB_BACTK	Q71sv7	bacillus	th	Q71sv7	bacillus	th	FT	VARIANT	352 F -> S (in strain EG5144).
147	245.5	7.2	633	2	Q71SV7	Q8ghf3	bacillus	th	Q8ghf3	bacillus	th	FT	VARIANT	417 VYF (in strain EG5144).
148	245.5	7.2	633	2	Q8GHF3	P21254	bacillus	th	P21254	bacillus	th	FT	VARIANT	451 S -> G (in strain EG5144).
149	245	7.2	633	1	C2AB_BACTK	Q7x2S7	bacillus	th	Q7x2S7	bacillus	th	FT	VARIANT	590 L -> I (in strain EG5144).
150	242	7.1	633	2	Q7X2S7	Q7x2S7	bacillus	th	Q7x2S7	bacillus	th	FT	VARIANT	600 K -> I (in strain EG5144).
												FT	HELIX	65 79
												FT	TURN	80 81
												FT	HELIX	83 86
												FT	TURN	87 88
												FT	HELIX	91 98
												FT	TURN	99 99
												FT	TURN	102 103
												FT	HELIX	105 113
												FT	TURN	114 114
												FT	HELIX	115 118
												FT	TURN	119 119
												FT	HELIX	124 124
												FT	HELIX	156 158
												FT	HELIX	161 181
												FT	HELIX	182 185
												FT	HELIX	188 189
												FT	HELIX	191 209
												FT	TURN	210 210
												FT	HELIX	211 215
												FT	HELIX	216 220
												FT	HELIX	223 254
												FT	HELIX	255 255
												FT	HELIX	260 276
												FT	TURN	277 277
												FT	HELIX	278 281

ALIGNMENTS

RESULT 1	C3BB_BACTU	STANDARD;	PRT;	652 AA.
ID	C3BB_BACTU			
AC	Q06177; Q45717;			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Pesticidal crystal protein cry3Bb (Insecticidal delta-endotoxin CryIIIb) (Crystalline entomocidal protoxin) (74 kDa crystal protein).			
DE	Name=cry3Bb; Synonyms=cryIIIb (b), cryIIIb2;			
GN	Bacillus thuringiensis.			
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OC	NCBI_TaxID=1428;			
OX	RA Donovan W.P., Rupar M.J., Slaney A.C., Maivar T., Gawron-Burke M.C., Johnson T.B.; "Characterization of two genes encoding Bacillus thuringiensis insecticidal crystal proteins toxic to Coleoptera species.";			
RN	[1]			
RP	SEQUENCE FROM N.A.			
	STRAIN=EG4961;			
	MEOLINE=93119147; PubMed=1476436;			
	RA Donovan W.P., Rupar M.J., Slaney A.C., Maivar T., Gawron-Burke M.C., Johnson T.B.; "Characterization of two genes encoding Bacillus thuringiensis insecticidal crystal proteins toxic to Coleoptera species.";			
	RT			

FT	TURN	283	Qy	241	TDHCYNNWYNGLNGIRSTYDAWYKFNRFREMTLTVDLIVLFFDYDIRLYSKVKTTEL
PT	HELIX	282	Db	241	TDHCYNNWYNGLNGIRSTYDAWYKFNRFREMTLTVDLIVLFFDYDIRLYSKVKTTEL
PT	TURN	284	Db	241	TDHCYNNWYNGLNGIRSTYDAWYKFNRFREMTLTVDLIVLFFDYDIRLYSKVKTTEL
PT	STRAND	289	Qy	301	TRDIFTDPISLNTLQEYGPFTLSENSIRKPHLFDYLOGIEFHTRLQPGYFGKHSFNYW
FT	STRAND	295	Db	301	TRDIFTDPISLNTLQEYGPFTLSENSIRKPHLFDYLOGIEFHTRLQPGYFGKHSFNYW
PT	TURN	304	Qy	301	TRDIFTDPISLNTLQEYGPFTLSENSIRKPHLFDYLOGIEFHTRLQPGYFGKHSFNYW
PT	TURN	313	Db	301	TRDIFTDPISLNTLQEYGPFTLSENSIRKPHLFDYLOGIEFHTRLQPGYFGKHSFNYW
PT	HELIX	316	Qy	361	SGNYVETRSPSIGSSKTTSPFYGDKSTEPVKLSDGQKVYRTTANTIDVAAWPNKGKVYLG
PT	HELIX	322	Db	361	SGNYVETRSPSIGSSKTTSPFYGDKSTEPVKLSDGQKVYRTTANTIDVAAWPNKGKVYLG
PT	TURN	327	Qy	361	SGNYVETRSPSIGSSKTTSPFYGDKSTEPVKLSDGQKVYRTTANTIDVAAWPNKGKVYLG
PT	STRAND	336	Db	361	SGNYVETRSPSIGSSKTTSPFYGDKSTEPVKLSDGQKVYRTTANTIDVAAWPNKGKVYLG
PT	TURN	348	Qy	421	VTKVDFSQYQQDDQNETSTOTYDSKRNNGHVSAQSDIDQLPPTDEPLEKAYSHQLNAYE
PT	TURN	351	Db	421	VTKVDFSQYQQDDQNETSTOTYDSKRNNGHVSAQSDIDQLPPTDEPLEKAYSHQLNAYE
PT	STRAND	354	Qy	421	VTKVDFSQYQQDDQNETSTOTYDSKRNNGHVSAQSDIDQLPPTDEPLEKAYSHQLNAYE
PT	STRAND	357	Db	421	VTKVDFSQYQQDDQNETSTOTYDSKRNNGHVSAQSDIDQLPPTDEPLEKAYSHQLNAYE
PT	TURN	357	Qy	481	CFLMQDRRGTTIPFTTWHSVDFNNTIDEKITOLPVVKAALGSASIEGPFTGGNL
PT	STRAND	371	Db	481	CFLMQDRRGTTIPFTTWHSVDFNNTIDEKITOLPVVKAALGSASIEGPFTGGNL
PT	STRAND	377	Qy	481	CFLMQDRRGTTIPFTTWHSVDFNNTIDEKITOLPVVKAALGSASIEGPFTGGNL
PT	STRAND	378	Db	481	CFLMQDRRGTTIPFTTWHSVDFNNTIDEKITOLPVVKAALGSASIEGPFTGGNL
PT	STRAND	382	Qy	481	CFLMQDRRGTTIPFTTWHSVDFNNTIDEKITOLPVVKAALGSASIEGPFTGGNL
PT	STRAND	383	Db	481	CFLMQDRRGTTIPFTTWHSVDFNNTIDEKITOLPVVKAALGSASIEGPFTGGNL
PT	TURN	391	Qy	481	CFLMQDRRGTTIPFTTWHSVDFNNTIDEKITOLPVVKAALGSASIEGPFTGGNL
PT	STRAND	396	Db	481	CFLMQDRRGTTIPFTTWHSVDFNNTIDEKITOLPVVKAALGSASIEGPFTGGNL
PT	STRAND	399	Qy	541	LFLKESSNSIAKPKVTLNSAALLQRYRIRYASTTNLRLFVONSNDPLVIVINKTMNK
PT	TURN	411	Db	541	LFLKESSNSIAKPKVTLNSAALLQRYRIRYASTTNLRLFVONSNDPLVIVINKTMNK
PT	STRAND	413	Qy	541	LFLKESSNSIAKPKVTLNSAALLQRYRIRYASTTNLRLFVONSNDPLVIVINKTMNK
PT	STRAND	414	Db	541	LFLKESSNSIAKPKVTLNSAALLQRYRIRYASTTNLRLFVONSNDPLVIVINKTMNK
PT	TURN	417	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	430	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	431	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	435	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	450	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	HELIX	455	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	HELIX	468	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	474	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	483	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	486	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	487	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	490	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	498	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	500	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	503	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	504	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	506	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	506	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	512	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	HELIX	517	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	519	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	522	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	525	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	526	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	527	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	540	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	543	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	551	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	HELIX	559	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	562	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	565	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	574	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	578	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	584	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	585	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	589	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	594	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	601	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	HELIX	606	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	610	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	613	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	618	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	625	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	TURN	636	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	640	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	STRAND	649	Db	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	SEQUENCE	652 AA;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	SEQUENCE	74385 MW;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	SEQUENCE	63048332 CD8BCCC6 CRC64;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	Query Match	100.0 %;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	Best Local Similarity	100.0 %;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	Matches	652;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	Conservative	0;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	Mismatches	0;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	Indels	0;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
PT	Gaps	0;	Qy	601	DDDLITYQPELATNSNMGSQDKNEELIGAESPVSNEKIYDKEIFIVQL
Db	1	MNPNNRSEDTIKWTPNSLQTHNQYPLADNNSTLBELNKTFEMLTDSSTEVDLNS	60	CC	-1 - SIMILARITY: Belongs to the delta endotoxin family.
Db	1	MNPNNRSEDTIKWTPNSLQTHNQYPLADNNSTLBELNKTFEMLTDSSTEVDLNS	60	CC	-1 -
Qy	61	TVKDAVGCGISVNGQIISGVGPFAGALTSPYQSFLNTIWPSADPKAFMAQVEVLIDK	120	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
Qy	61	TVKDAVGCGISVNGQIISGVGPFAGALTSPYQSFLNTIWPSADPKAFMAQVEVLIDK	120	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
Db	61	TVKDAVGCGISVNGQIISGVGPFAGALTSPYQSFLNTIWPSADPKAFMAQVEVLIDK	120	CC	the European Bioinformatics Institute. There are no restrictions on its
Qy	121	KIEEYAKSKALAELQGLQNINFEDVNALNSWKTPLSLRSRSQDRTRLEFSQAESHFRN	180	CC	use by non-profit institutions as long as its content is in no way
Db	121	KIEEYAKSKALAELQGLQNINFEDVNALNSWKTPLSLRSRSQDRTRLEFSQAESHFRN	180	CC	modified and this statement is not removed. Usage by and for commercial
Qy	181	SMPFAVSKFEVFLPFTAQANTHLLJKDACYFGEWMGYSSDEVAEFYHRQLKTQQY	240	CC	entities requires a license agreement (See http://www.iab-sib.ch/announce/)
Db	181	SMPFAVSKFEVFLPFTAQANTHLLJKDACYFGEWMGYSSDEVAEFYHRQLKTQQY	240	CC	or send an email to license@iab-sib.ch).
DR	X17123; CAA34983.1; -		CC	-1 -	
DR	EMBL; A07234; CAA00645.1; -		CC	-	
DR	PIR; S10228; S10228.		CC	-	
DR	HSSP; 006117; 1J76		CC	-	
DR	InterPro; IPR001178; Endotoxin.		CC	-	

DR	InterPro; IPR005638; endotoxin C.	OX	NCBI_TaxID=1444, 1441, 1435;
DR	InterPro; IPR005639; endotoxin N.	RN	[1] SEQUENCE FROM N.A.
DR	InterPro; IPR008979; Gal bind Like.	RP	SPECIES=B.t.tenebrionis;
DR	Pfam; PF03944; Endotoxin C; 1-	RC	MEDLINE=88015559; PubMed=3658680;
DR	Pfam; PF00555; Endotoxin_M; 1.	RX	RT
DR	Pfam; PF03945; Endotoxin_N; 1.	RA	Hoefft H., Seurinck J., Houven A.V., Vaect M.;
KW	Sporulation; Toxin; Sequence; 659 AA; 75159 MW; 5A5B214PF84168CA CRC64;	RA	"Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus thuringiensis var. tenebrionis toxic against Coleoptera.";
SQ	SEQUENCE	RL	Bacillus thuringiensis var. tenebrionis. Nucleic Acids Res. 15:7183-7183(1987).
Query Match	94.3%; Score 3212; DB 1; Length 659;	RL	[2]
Best Local Similarity	93.7%; Pred. No. 1.2e-201;	RN	SEQUENCE FROM N.A.
Matches	610; Conservative 22; Mismatches 19; Indels 0; Gaps 0;	RP	SPECIES=B.t.tenebrionis;
Qy	1 MNPNRSEHDTIKVTNPSELQTNHNOYPLADNPNSTLEELNYKEPLRMTDSSTEVLDNS 60	RC	SEKAR V., Thompson D.V., Maroney M.J., Bookland R.G., Adang M.J.;
Db	9 MNPNRSEHDTIKVTNPSELQTNHNOYPLADNPNSTLEELNYKEPLRMTDSSTEVLDSS 68	RA	"Molecular cloning and characterization of the insecticidal crystal protein gene of Bacillus thuringiensis var. tenebrionis.";
Qy	61 TVKDAYTGISVGVQIQLGVYPPFAGALTSPYQSFNTINPSDADPKMAQVEVLIDK 120	RT	Proc. Natl. Acad. Sci. U.S.A. 84:7036-7040(1987).
Db	69 TVKDAYTGISVGVQIQLGVYPPFAGALTSPYQSFNTINPSDADPKMAQVEVLIDK 128	RL	[3]
Qy	121 KIEEYAKSKALAELQGQNFDYVNLNSWIKTPLSRSKRSQDIREFSQAESHPRN 180	RP	SEQUENCE FROM N.A.
Db	129 KIEEYAKSKALAELQGQNFDYVNLNSWIKTPLSRSKRSQDIREFSQAESHPRN 188	PC	SPECIES=B.t.tenebrionis;
Qy	181 SMPSFAVSKFEVFLFLPTYQAQANTHLILKDAQVGEWGYSSVEDAEFYTHROLKLTOQY 240	RA	Fischhoff D.A.; McPherson S.A., Perlak F.J., Fuchs R.L., Marrone P.G., Lavrik P.B.,
Db	189 SMPSFAVSKFEVFLFLPTYQAQANTHLILKDAQVGEWGYSSVEDAEFYTHROLKLQQY 248	RX	"Characterization of the coleopteran-specific protein gene of Bacillus thuringiensis var. tenebrionis.";
Qy	241 TDHCVNWYNGNGLRGSTDYDAWKVNFREREMTITVLDLIVLFPEFYDIRLYSKGVKTTEL 300	RA	Biotechnology (N.Y.) 6:61-66(1988).
Db	249 TDHCVNWYNGNGLRGSTDYDAWKVNFREREMTITVLDLIVLFPEFYDIRLYSKGVKTTEL 308	RL	[4]
Qy	301 TRDIFDPFISLNTLOYPGPFLSIENSIKRPHFLDYLOGEFPHTRLQGYFGKDFSNYW 360	RN	SEQUENCE FROM N.A.
Db	309 TRDIFDPFIFTNLQEQGPFISSIENSIKRPHFLDYLGIEFHTRLQGYFGKDFSNYW 368	PC	SPECIES=B.t.moriori; STRAIN=NB176;
Qy	361 SGNYVTRPSTGSSKTKITSPPYGDKSTEPVOKLTSFQDKQYKRTIANTDVAAPNGKRYLG 420	RX	MEDLINE=95131759; PubMed=7830581;
Db	369 SGNYVTRPSTGSSKTKITSPPYGDKSTEPVOKLTSFQDKQYKRTIANTDVAAPNGKRYLG 420	RA	Adams L.P., Mathews S., O'Hara P., Petersen A., Gurtler H.;
Qy	421 VTKVDFSOYDDKNETSTQTYDSKRKNHGSQDSDQLPPTTDEPLEKASHOLNAYE 480	RT	"Elucidation of the mechanism of Cry2IAA overproduction in a mutantized strain of Bacillus thuringiensis var. tenebrionis.";
Db	429 VTKVDFSOYDDKNETSTQTYDSKRKNHGSQDSDQLPPTTDEPLEKASHOLNAYE 488	RL	RT
Qy	481 CPIMODRGTIPFPTWHSIDFENTIDAEKTTOLPVKAALSSASIEFGPGFTGGNL 540	RN	RT
Db	489 CPIMODRGTIPFPTWHSIDFENTIDAEKTTOLPVKAALSSASIEFGPGFTGGNL 548	PC	RT
Qy	541 LPUKESSNSIAKEPVTLNSAALLQFVRIVASTNLRLFVQNSNDPLFVYINTKTMNK 600	RX	RT
Db	549 LPUKESSNSIAKEPVTLNSAALLQFVRIVASTNLRLFVQNSNDPLFVYINTKTMNK 608	RA	RT
Qy	601 DDPLTYOFTPLATTSNSNNGFSGDNKELIIGAESFSVNEKUYIDKIEFIPVQ 651	RT	RT
Db	609 DDPLTYOFTPLATTSNSNNGFSGDNKELIIGAESFSVNEKUYIDKIEFIPVQ 659	CC	Nature 353:815-821(1991).
RESULT	3	CC	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
C3AA_BACTT	ID_C3AA_BACTT STANDARD;	CC	SPECIES=B.t.tenebrionis;
AC	P01130; P21255;	CC	MEDLINE=92049739; PubMed=1658659; DOI=10.1038/353815a0;
DT	01-APR-1988 (Rel. 07, Created)	CC	-I- FUNCTION: Promotes colloidiosmotic lysis by binding to the midgut epithelial cells of Coleoptera.
DT	25-OCT-2004 (Rel. 45, Last annotation update)	CC	-I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
DE	Pesticidal crystal protein cry3Aa precursor (Insecticidal delta-endotoxin Cry3Aa) (Crystalline entomocidal protoxin) (73 kDa crystal protein).	CC	-I- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in Insect-resistant potato by Monsanto.
DE	Name=cry3Aa; Synonyms=bt13, cry3A, cryC, cryIIIA(a);	CC	-I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
DE	Bacillus thuringiensis (subsp. morrisonii), and Bacillus thuringiensis (subsp. san diego),	CC	-I- SIMILARITY: Belongs to the delta endotoxin family.
GN	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus	CC	-----
OS	Bacillus thuringiensis (subsp. tenebrionis),	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
OS	Bacillus thuringiensis (subsp. san diego), and	CC	the European Bioinformatics Institute. There are no restrictions on its
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus	CC	

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CC EMBL; Y00420; CAA64482.1; -
 CC EMBL; M3207; AAA22541.1;
 CC EMBL; U01985; AAC03266.1; -
 DR EMBL; M40503; AAA22542.1;
 DR EMBL; M22472; AAA22336.1; ALT_INIT.
 PDB; 1DLC; X-ray; @=61-644.
 InterPro; IPR00118; Endotoxin.
 InterPro; IPR00568; endotoxin_C.
 InterPro; IPR00569; endotoxin_N.
 InterPro; IPR00899; Gal_bird_Like.
 DR Pfam; Pro3944; Endotoxin_C; 1.
 DR Pfam; Pro00555; Endotoxin_M; 1.
 DR Pfam; Pro3945; Endotoxin_N; 1.
 KW 3D-structure; Genetically modified food; Sporulation; Toxin.
 PROSP 1
 FT CHAIN 58 644
 FT CONFLICT 544 644
 FT HELIX 63 76
 FT TURN 77 78
 FT STRAND 81 81
 FT HELIX 85 98
 FT TURN 99 99
 FT HELIX 103 117
 FT TURN 118 118
 FT HELIX 123 152
 FT TURN 155 156
 FT HELIX 160 180
 FT HELIX 181 184
 FT TURN 187 188
 FT TURN 190 193
 FT HELIX 194 214
 FT TURN 215 219
 FT HELIX 222 253
 FT TURN 254 254
 FT HELIX 259 275
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 FT HELIX 277 280
 FT TURN 281 282
 FT HELIX 283 286
 FT TURN 288 288
 FT STRAND 294 296
 FT STRAND 302 304
 FT HELIX 315 316
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 FT STRAND 335 347
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 FT STRAND 390 393
 FT TURN 395 396
 FT STRAND 398 411
 FT TURN 412 413
 FT STRAND 414 428
 FT STRAND 429 432
 FT STRAND 433 440
 FT STRAND 447 451
 FT HELIX 452 454
 FT TURN 455 455
 FT HELIX 465 468
 FT STRAND 471 480
 FT HELIX 482 484
 FT STRAND 487 495
 FT TURN 496 497

Removed in mature form.
 Pesticidal crystal protein cry3Aa.
 G -> A (in Ref. 3).

SEQ	SEQUENCE	AA:	73108 MW;	EFCOFFICECEFA9683 CRC64;
QY	1	MNPNNRSRHDITKTVTPNSELQTHNQYPLADVNSTLEELNYKEPLMTEDSSTEVDNS	60	Query Match
Db	1	MNPNNRSRHDITKTTENNEVPTNHOVPLAETNPNTLEDLNKTFELRTADNTEADSS	60	Best Local Similarity
QY	61	TVKDAVGIGISVQIUGUVGVPPAGALTSPYOSFLNTIWPSPADPKAFMAQEVLIDK	120	Matches 446; Conservative
Db	61	TRKDVIQKGISVQGDLLGVGPFGGALVSFTNLNTIWPE-DPKAFMEQEVALMDQ	119	Score 2341.5; DB 1; Length 644;
QY	121	KIBBYAKSKAELBQLGQNNEFDYVNALNSWCKTPLSLRSRSQRDRLELFSONESHPRN	180	Prod. No. 1e-144; Indels 7; Gaps 6;
Db	120	KIADYAKNKAKAELBQLGQNNEVDYVSAISWQKNPVSSRNPHSGQRLEFSAESHFRN	179	Score 68.7; DB 1; Length 644;
QY	181	SMPSFAVSKFEVILFLPYAQAAANTHLLKKDQVFGVQFGEWGSSEDVAFYHQLKTQY	240	Score 68.6; DB 1; Length 644;
Db	180	SMPSFAISGYEVILFLTYAQAAANTHLLFKDQIYGEEWGYEKEDIAEFYKRLQKLQTQY	239	Score 68.6; DB 1; Length 644;
QY	241	TDHCVNWNVNGLRLSTYDAWKFRFRRENTLTLDLIVLPFDIRLYSKGVKTBL	300	Score 68.6; DB 1; Length 644;
Db	240	TDHCVKVNNVGLDKLRGSSYESKWNFNFRYRRENTLTVDLIAFLPFLDVLKFKEVKTBL	299	Score 68.6; DB 1; Length 644;
QY	301	TRDIFTDPIFSINTLQEYGPFTLSIENSIRKPHLFYDLYQIEFHTRLQGPYFGKDSFNYW	360	Score 68.6; DB 1; Length 644;
Db	300	TRDVLTDPIGVNNLRLGYGTFSNIENYIRKPHLFYLHQTRLQGPYGNDSFNYW	359	Score 68.6; DB 1; Length 644;
QY	361	SGNYVETRPSIGSSKTTTSPFGDKSTEPVQLSFDSGKVYRTIANTDVAAVPGNGKYLG	420	Score 68.6; DB 1; Length 644;
Db	360	SGNYVSTRPSISNDITTSPPVGNKSSPVQNLEFNGKVRAVANTLAVWPSA-YVSG	418	Score 68.6; DB 1; Length 644;
QY	421	VTKVDFSOYDDQKNETSTOTIDSKRKNHGVSAQSDSIOLPPETTDEPLEKAYSHOLNVAE	480	Score 68.6; DB 1; Length 644;
Db	419	VTKVFEVSQYNDQTDQTAQTVDSKRKNYAVS-WDSIQLQPPETTDEPLEKGVSHQLNYYVM	477	Score 68.6; DB 1; Length 644;
QY	481	CFLMQDRGTIPFFWTRSYDFFNTIDAEEKITQLPVVKAYALSSASTIEGPGFTGPNL	540	Score 68.6; DB 1; Length 644;
Db	478	CFLMQGSRGTTIPVLTWTHSKVDFNMIDSKitQPLVKAYKLQSGASVAGPRTGSDI	537	Score 68.6; DB 1; Length 644;
QY	541	LPEKKESSNSIAKPKVNTNSAALLQRRVRIRASTMLRLFVQNSNNDFLVITYINKTANK	600	Score 68.6; DB 1; Length 644;
Db	538	IQCTE-NGSAATIVYT-PDVTSQKTRARIYASTSQTFTFUSLGDAPNQYFDKTINK	595	Score 68.6; DB 1; Length 644;
QY	601	DDDLTQTFDLATINSIMMGFSSDKNELLIGAESFSVNEKIDKIERIPV	650	Score 68.6; DB 1; Length 644;
Db	596	GDTLRTNSFNLAASFSTPFELSG--NNLQIGVTGLSAQDKVYIDKIEPFPV	643	Score 68.6; DB 1; Length 644;

Q9S6N9	PRELIMINARY;	PRT;	652 AA.
AC			
DT	01-MAY-2000 (T-TREMBrel. 13, Created)		
DT	01-MAY-2000 (T-TREMBrel. 13, Last sequence update)		
DT	01-MAR-2004 (T-TREMBrel. 26, Last annotation update)		
DE	Cry3aa protein.		
GN	Name=CRY3AA;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BT22;		
RA	Zhang J., Song F.P., Xie T.J., Wang K.M., Huang D.F.;		
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ231900; CAB41411.1; -.		
PIR	A27323; A27323.		
DR	HSSP; P07130; IDLC.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:000512; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
InterPro	IPR001178; Endotoxin.		
InterPro	IPR005638; endotoxin_C.		
InterPro	IPR005639; endotoxin_N.		
InterPro	IPR008979; Gal_bind_Like.		
DR	PFAM; PF03944; Endotoxin_C; 1.		
DR	PFAM; PF00555; Endotoxin_M; 1.		
DR	PFAM; PF003945; Endotoxin_N; 1.		
DR	SEQUENCE 652 AA; 74035 MW;	544AE16EDDF7647 CRC64;	
Query Match	68.6%; Score 2341.5; DB 2; Length 652;		
Best Local Similarity	68.6%; Pred. No. 1.1e-144;		
Matches	446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;		
Db	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
Qy	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
Db	61 TVKDAVGTVGIVQGIIQGVPGAGLTSFVQSFNTIWPSDADPKWAKFAQVEVLI 120		
Qy	61 TVKDAVGTVGIVQGIIQGVPGAGLTSFVQSFNTIWPSDADPKWAKFAQVEVLI 120		
Db	69 TTKDVIQKGISVGVDLGVGVPFGGALVFSYTNTWPE-DPWKWAKFQEVAEMLDQ 127		
Qy	69 TTKDVIQKGISVGVDLGVGVPFGGALVFSYTNTWPE-DPWKWAKFQEVAEMLDQ 127		
Db	121 KIEEYAKSKAKAELQGLQNFDYYNALSWKTKPLSLRSKRSQRDRRELPSQAESHFRN 180		
Qy	121 KIEEYAKSKAKAELQGLQNFDYYNALSWKTKPLSLRSKRSQRDRRELPSQAESHFRN 180		
Db	128 KADYAKNKAALQGLQNVDYVSAISWQKNPVSSRNPHSQGRRELPSQAESHFRN 187		
Qy	128 KADYAKNKAALQGLQNVDYVSAISWQKNPVSSRNPHSQGRRELPSQAESHFRN 187		
Db	181 SMPSFAVKSEFLPLTYAQAANTHLILKDQVFGBEWGSSEDVAEFTHQLKLHQX 240		
Qy	181 SMPSFAVKSEFLPLTYAQAANTHLILKDQVFGBEWGSSEDVAEFTHQLKLHQX 240		
Db	188 SMPSFAISGEVFLTLTYAQAANTHLFLKDQIYGEBMWGEKEKEDAEFYKQLKLHQX 247		
Qy	188 SMPSFAISGEVFLTLTYAQAANTHLFLKDQIYGEBMWGEKEKEDAEFYKQLKLHQX 247		
Db	241 TDHCVNWNVGLNGLRSGYTDAMKENFRREMTLVLDLIVLFPPYDLYSKGYKTEL 300		
Qy	241 TDHCVNWNVGLNGLRSGYTDAMKENFRREMTLVLDLIVLFPPYDLYSKGYKTEL 300		
Db	248 TDHCVKWVNGVGLDKLRGSSEYVNFYRREMTLVLDLIVFLPYDLYSKGYKTEL 307		
Qy	248 TDHCVKWVNGVGLDKLRGSSEYVNFYRREMTLVLDLIVFLPYDLYSKGYKTEL 307		
Db	301 TRDIFTDPFLSANTLQEVGPTFLSISIENSRKPHLPFLDYLQGIFHTRIQLQGYFKGDSENW 360		
Qy	301 TRDIFTDPFLSANTLQEVGPTFLSISIENSRKPHLPFLDYLQGIFHTRIQLQGYFKGDSENW 360		
Db	308 TRDVLTDPPVGUNNLRGYGTTFNENYRKPHLPFLDYLQGIFHTRIQLQGYFKGDSENW 367		
Qy	308 TRDVLTDPPVGUNNLRGYGTTFNENYRKPHLPFLDYLQGIFHTRIQLQGYFKGDSENW 367		
Db	421 VTKVDFSQDDQNETSTOTYDKKRNNCHVSADSIOLPPETTDEPLEKAYSHQNYAE 480		
Qy	421 VTKVDFSQDDQNETSTOTYDKKRNNCHVSADSIOLPPETTDEPLEKAYSHQNYAE 480		
Db	427 VTKVDFSQNDQTDEASTCYDKRNNCVAVAS-WDSIDOLPPETTDEPLEKAYSHQNYVM 485		
Qy	427 VTKVDFSQNDQTDEASTCYDKRNNCVAVAS-WDSIDOLPPETTDEPLEKAYSHQNYVM 485		
Db	481 CPMQDRRTIPFPTWHSVDFNTIDEAKITOLPVLKAYAASSGASIEPGFTGGNL 540		
Qy	481 CPMQDRRTIPFPTWHSVDFNTIDEAKITOLPVLKAYAASSGASIEPGFTGGNL 540		
Db	486 CPMQGSRRTIPVLTWTHKSDFKQVYRVTIANTDVAAMPNGKVYLG 420		
Qy	486 CPMQGSRRTIPVLTWTHKSDFKQVYRVTIANTDVAAMPNGKVYLG 420		
Db	541 LFLKESSNSPIAKFKVTLNSAAILQRYVRIRYASTNLRFLVONSNNDFLVYINKTMNK 600		
Qy	541 LFLKESSNSPIAKFKVTLNSAAILQRYVRIRYASTNLRFLVONSNNDFLVYINKTMNK 600		
Db	546 IOCIE-NGSATIIVYT-PDVSVSQKYARIHYASTSSQTITFTLSLDGAPFNQYFDKTINK 603		
Qy	601 DDDLTYQFQFDLATNSNMGFSGKRNELLIGASEFVSNKEKIXIDKIEFELPV 650		
Db	604 GDTLTYNSENLAStSPPFELSG--NNLQGVTGLSAGDKVYDKEFELPV 651		
RESULT 5			
Q6PBN8	PRELIMINARY;	PRT;	652 AA.
ID	Q6PBN8;		
AC	AC_06PBN8;		
DT	05-JUL-2004 (TREMBrel. 27, Created)		
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBrel. 27, Last annotation update)		
DB	DB_Insecticidal_crystal_protein.		
GN	Name=cry3;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
NCBI_TaxID	1428;		
RC	SEQUENCE FROM N.A.		
RA	STRAIN=BT22;		
RA	Zhang J., Song F.P., Xie T.J., Wang K.M., Huang D.F.;		
RA	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AJ231900; CAB41411.1; -.		
DR	EMBL; AJ231900; CAB41411.1; -.		
DR	PIR; A27323; A27323.		
DR	HSSP; P07130; IDLC.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0009405; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	GO; GO:0006932; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR011178; Endotoxin.		
DR	InterPro; IPR005639; endotoxin_C.		
DR	InterPro; IPR008979; Gal_bind_Like.		
DR	PFAM; PF03944; Endotoxin_C; 1.		
DR	PFAM; PF00555; Endotoxin_M; 1.		
DR	PFAM; PF003945; Endotoxin_N; 1.		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
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DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
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DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
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DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
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DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
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DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
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Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
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Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
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DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
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DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;		
DR	1 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	9 MNPNNRSEHTDTIKVTNPSELQTNHNNQYPLADNPNSTLEELVNYKEFLRMTDSSTEVLDSN 60		
DR	SEQUENCE 652 AA; 74007 MW; AC2756FDDED104A45 CRC64;		
Query Match	68.6%; Score 2337.5; DB 2; Length 652;		
Best Local Similarity	68.5%; Pred. No. 1.9e-144;		
Matches	445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;</td		

Qy	481	CFLMODRRGRIPPFWTHRSYDFENTIDEAKITQLPVVKAYAASSGASLIEGPOFTGGNL	540	Db	486	CFLMQGSRGTRTIPVPLTWTHKSVDPFNMIDSKKITQLPVKLOSSGASVVGPRPTGGDI	545		
Db	486	CFLMQGSRGTRTIPVPLTWTHKSVDPFNMIDSKKITQLPVKLOSSGASVVGPRPTGGDI	545	Qy	541	LFLKESSNSIAKPKVTLNSAALLQYRVRIRYASTNTNLPEVQNSNNDLVLIVINKTMNK	600		
Qy	541	LFLKESSNSIAKPKVTLNSAALLQYRVRIRYASTNTNLPEVQNSNNDLVLIVINKTMNK	600	Db	546	IQCITE-NGSAATIYT-PDVSYSQKRHRHYASTSQITFTLSIDGAPNQYYFDKTINK	603		
Db	546	IQCITE-NGSAATIYT-PDVSYSQKRHRHYASTSQITFTLSIDGAPNQYYFDKTINK	603	Qy	601	DDDLTYQPFDLATNSNNMGSGDKNEELIGAESFSVSNKVIYDKEIFPV	650		
Qy	601	DDDLTYQPFDLATNSNNMGSGDKNEELIGAESFSVSNKVIYDKEIFPV	650	Db	604	GDTLTYNSEFLASFSTPFEELSG--NNLQIGVTSLSAGDKVYIDKEIFPV	651		
Db	604	GDTLTYNSEFLASFSTPFEELSG--NNLQIGVTSLSAGDKVYIDKEIFPV	651	RESULT 7					
				C3CA_BACTK					
				ID _C3CA_BACTK					
				AC 045744;					
				DT 30-MAY-2000 (Rel. 39, Created)					
				DT 30-MAY-2000 (Rel. 39, Last sequence update)					
				DT 05-JUL-2004 (Rel. 44, Last annotation update)					
				DB Pesticidal crystal protein cry3C (Insecticidal delta-endotoxin)					
				DE Cry3Ca1) (Crystalline entomocidal protein) (73 kDa crystal protein).					
				GN Name=cry3Ca; Synonyms=cryIIIC(a), cryIIID,					
				OS Bacillus thuringiensis (subsp. kurstaki).					
				OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.					
				RN NCBI_TaxID=29339;					
				RN [1]					
				RP SEQUENCE FROM N.A.					
				RC STRAIN=BTT109P;					
				RX PMID=192184108; PubMed=1544571; DOI=10.1016/0378-1119(92)90457-2;					
				RA Lambert B., Theunis W., Aguda R., Van Audenhove K., Decock C.,					
				RA Jansens S., Smeirinck J., Peferoen M.;					
				RT "Nucleotide sequence of gene cryIIID encoding a novel coleopteran active crystal protein from strain BTT109P of Bacillus thuringiensis subsp. kurstaki".					
				RT Gene 110:131-132 (1992).					
				RL					
				CC -1- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of Coleoptera.					
				CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.					
				CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.					
				CC -1- SIMILARITY: Belongs to the delta endotoxin family.					
				CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities require a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
				CC EMBL: X59797; CAR42469.1; -.					
				DR PIR: JH0261; JH0261.					
				DR HSSP: P07130; IDIC.					
				DR InterPro: IPR01178; Endotoxin.					
				DR InterPro: IPR05638; endotoxin C.					
				DR InterPro: IPR05639; endotoxin N.					
				DR InterPro: IPR08979; Gal-bind_Tike.					
				DR Pfam: PF03944; Endotoxin_C; 1.					
				DR Pfam: PF00555; Endotoxin_M; 1.					
				DR Pfam: PF03945; Endotoxin_N; 1.					
				KW Sporulation>Toxin.					
				SQ SEQUENCE 649 AA; 73026 MW; BFP1FOB47957AC49 CRC64;					
				Query Match 63.2%; Score 2152; DB 1; Length 649;					
				Best Local Similarity 62.2%; Pred. No. 2, 7e-132;					
				Matches 407; Conservative 95; Mismatches 142; Indels 10; Gaps 6;					
Qy	1	MNPNNRSEDTIKTPNSLOTHNQNQPHADPNSTLFLNEYKEFLMTEDSSTEVLNDS	60	Db	1	MNPNNRSEDTIKTPNSLOTHNQNQPHADPNSTLFLNEYKEFLMTEDSSTEVLNDS	60		
Db	9	MNPNNRSEDTIKTPNSLOTHNQNQPHADPNSTLFLNEYKEFLMTEDSSTEVLNDS	60	Qy	1	MNPNNRSEDTIKTPNSLOTHNQNQPHADPNSTLFLNEYKEFLMTEDSSTEVLNDS	60		
Qy	1	TWDAVGTJSWVQQLGVGPPAGALTSPYQSPLNTWPSADPKMAQVEVLIDK	120	Db	9	TTKDQVQKTSWVGLGPFLLGTVGFPGVGLAVSFYTNFLNTWPS-EPMKAQVEALMDQ	127		
Db	9	TWDAVGTJSWVQQLGVGPPAGALTSPYQSPLNTWPSADPKMAQVEVLIDK	120	Qy	121	KIEEYAKSKAKAELQGLQNFDYDYNALNSWKTPLSLRSKRSQDRTRLEFLSOAESFRN	180		
Qy	121	KIEEYAKSKAKAELQGLQNFDYDYNALNSWKTPLSLRSKRSQDRTRLEFLSOAESFRN	180	Db	128	KIADYKWKAKAELQGLQNINVDEVSLWSQKNPVSSRNPHSQGRIRLEFLSOAESFRN	187		
Db	128	KIADYKWKAKAELQGLQNINVDEVSLWSQKNPVSSRNPHSQGRIRLEFLSOAESFRN	187	Qy	181	SMPEFAVSPFEVLPLTYPAQAAANTHLFLRDAQIYGEVDYAEFYKROLKTCQY	240		
Qy	181	SMPEFAVSPFEVLPLTYPAQAAANTHLFLRDAQIYGEVDYAEFYKROLKTCQY	240	Db	188	SMPSFAISVEVLRLTQAQAAANTHLFLRDAQIYGEVDYAEFYKROLKTCQY	247		
Db	188	SMPSFAISVEVLRLTQAQAAANTHLFLRDAQIYGEVDYAEFYKROLKTCQY	247	Qy	241	TDHCVNWTNGVNLGLRGSSTDANTKENRPRRENTLVLDLIVLFFDIRLYSKGVTEL	300		
Qy	241	TDHCVNWTNGVNLGLRGSSTDANTKENRPRRENTLVLDLIVLFFDIRLYSKGVTEL	300	Db	248	TDHCVKWNVGLDKLURGSYESWNENYRRENTLVLDLIALFPLYDVLRLPEKEVTEL	307		
Db	248	TDHCVKWNVGLDKLURGSYESWNENYRRENTLVLDLIALFPLYDVLRLPEKEVTEL	307	Qy	301	TRDIFTDPFLSLNTLQEQYOPTFUSIESTRKPHLFDFYLQGIEFPHTRLOGYFGRDSFNYW	360		
Qy	301	TRDIFTDPFLSLNTLQEQYOPTFUSIESTRKPHLFDFYLQGIEFPHTRLOGYFGRDSFNYW	360	Db	308	TRDVLTDPIVGVNVLRGYCTTSFNIENYTRKPHLFDFYLRIQFTRFPGYGNDSFNYW	367		
Db	308	TRDVLTDPIVGVNVLRGYCTTSFNIENYTRKPHLFDFYLRIQFTRFPGYGNDSFNYW	367	Qy	361	SGNYVETRSIGSKTISPFYGBKSTEVQKLSDQDQNETSTQYDCKTQYRVTANTDVAAPNGKVYLG	420		
Qy	361	SGNYVETRSIGSKTISPFYGBKSTEVQKLSDQDQNETSTQYDCKTQYRVTANTDVAAPNGKVYLG	420	Db	368	SGNYVSTRSIGSDINTSPYGNKSSSEVQNLJFENGVEYRAVANTLNWPSA-VYSG	426		
Db	368	SGNYVSTRSIGSDINTSPYGNKSSSEVQNLJFENGVEYRAVANTLNWPSA-VYSG	426	Qy	421	VTKVDFQSQQDDQNETSTQYDCKTQYRVTANTDVAAPNGKVYLG	480		
Qy	421	VTKVDFQSQQDDQNETSTQYDCKTQYRVTANTDVAAPNGKVYLG	480	Db	422	VTKVBFSSQNDQTDBASTQYDCKTQYRVTANTDVAAPNGKVYLG	485		
Db	422	VTKVBFSSQNDQTDBASTQYDCKTQYRVTANTDVAAPNGKVYLG	485	Qy	481	CFLMDQRRTIPFPTWTHRSYDFENTIDEAKITQLPVVKAYAASSGASLIEGPOFTGGNL	540		
Qy	481	CFLMDQRRTIPFPTWTHRSYDFENTIDEAKITQLPVVKAYAASSGASLIEGPOFTGGNL	540						

RC	STRAIN=NRRL B-18746 / PS50C;	Qy	512 ITQLEPVVKAYALSSASITIIGPPTGGNNLFLKSSNSN-AKFKVTLNSALLQARYVRV1
RA	Sick J.M., Sick A.J., Poncerada L.; "Novel coleopteran-active Bacillus thuringiensis isolate and a novel RT gene encoding a coleopteran-active toxin.";	Db	526 ITQIFAVKGDMYLUGGSVVIQGPFGGGDI -LRTPNSLIIGTFAVTNV-GSLSQYRVR1 582
RT	Patent number EP0498537, 12-AUG-1992.	Qy	571 RYASTTNLR-LFVONS--NNDFLVIVTKTMNDDTYQTDFLATINSNMGFEGDKNE 626
RL	-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of Coleoptera.	Db	583 RYASTTDPEFTLYDGTIEKMR--NRTMDNGASLYTEFKASFITDFQPFTQD 637
CC	-I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	Qy	627 LIIGAESFSNEKLYIDKIEFIPV 650
CC	-I- MISCELLANEOUS: Toxic segment of the protein is located in the N- terminus.	Db	638 ILLSNQDESSGQEYVYDRIEFIGV 661
CC	-I- SIMILARITY: Belongs to the delta endotoxin family.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RESULT 10	
DR	EMBL; U04364; AAA21117.1;	C8BA_BACULI	PRT; 1169 AA.
DR	HSSP; P01130; 1DLC.	ID C8BA_BACUL	STANDARD;
DR	InterPro; IPR001178; Endotoxin.	AC Q45705;	PRT; 1169 AA.
DR	InterPro; IPR005638; endotoxin_C.	DT 16-OCT-2001 (Rel. 40, Created)	
DR	InterPro; IPR005639; endotoxin_N.	DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DR	InterPro; IPR008979; Gal_bind_Like.	DT 05-JUL-2004 (Rel. 44, Last annotation update)	
DR	Pfam; PF03944; Endotoxin_C; 1.	DE Pesticidal crystal protein cryBa (insecticidal delta-endotoxin DE protein).	
DR	Pfam; PF00555; Endotoxin_M; 1.	DE CryIIIB(a) (Crystalline entomocidal protoxin) (134 kDa crystal protein).	
DR	Pfam; PF03945; Endotoxin_N; 1.	DE Name=cryBa; Synonyms=50C(b), cryVIIIB(a);	
KW	SEQUENCE: Toxin.	OS Bacillus thuringiensis (subsp. kumamotoensis).	
SQ	SEQUENCE: 11.57 AA; 131009 MW; 687B5C49DB9368JB CRC64;	OC Bacteria; Firmicutes; Bacillales; Bacilliaceae; Bacillus.	
Query Match	35.4%; Score 1205 5; DB 1; Length 1157;	RN [1]	
Best Local Similarity	39.2%; Pred. No. 5.3e-70;	RN [1]	
Matches	268; Conservative 135; Mismatches 224; Indels 57; Gaps 21;	RP SEQUENCE FROM N.A.	
Qy	1 MNPNRNRSEDTIKTPNSLQTNENQYPADNPNSTLPLNLYKEFLRMTEDSSTEVLDS 60	RC STRAIN=NRRL B-18746 / PS50C;	
Db	1 MSPNNQNVEELIDATPSVSVSDNRYPANEPTDALQMNYYKDLYKNSGGENPELFGNP 60	RA Michaels T.E., Foncerra L., Narva K.B.;	
Qy	61 TV--KDAVGTGIVGTGIVGRILGALGVPAQIAFYSF1VQLWPSKVDTIWBTMERVE 116	RC Bacteria; Firmicutes; Bacillales; Bacilliaceae; Bacillus.	
Db	61 ETPISSSTTQGTTGIGIVGRILGALGVPAQIAFYSF1VQLWPSKVDTIWBTMERVE 120	NCBI_TaxID: 132267;	
Qy	117 LIDKIEEYAKSKALAELQGLQNNFEDYNALNSWKCTPLSRSKRSQDIRELFSQES 176	RN [1]	
Db	121 LVDQRIEKVTKDKAELKGQNLADVYQSLDMLW--NRNDARTRSSVSNQFIALD 177	RT SEQUENCE ISOLATES;	
Qy	177 HFRNSMSPAVSKPSKEVLFLPETYQAQANTLULLKDAQVGEENGYSSVEDAEPYHQLKL 236	RL Patent number WO9315206, 05-AUG-1993.	
Db	178 NFVSSIPSPAVSGHEVLLLAVYAQAVNLHILLRDAISGEENGTPGEISRYNRQVL 237	CC -I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects. Active on various scarabaeid beetles.	
Qy	237 TQQYTDHCYKLNGLRGSTYDAWKXFNPFREMTLVDLIVLFLVPLFVYDRLYSKGV 296	CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	
Db	238 TABESDYCKWKYK1GLDKKKGTSKSWLWYHQFREMTLVLVDLVALFNFYDTHMPJET 297	CC -I- SIMILARITY: Belongs to the delta endotoxin family.	
Qy	297 KTELTRDIFTDP1-FSLNTLQEQ-----GPTFLSIENS-IRKPHFLFDYLOGIEFHT 346	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
Db	298 TAQQLTRDVTDP1AFNIVVSTGFCNPWSTHSGLFYEVENVTRPFLDLSSEVENTS 357	CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	
Qy	347 LQPGYFGKOF-NWWSGNVETRPSIGSSKTISPFYGDKSSTEPVQKUSF-----DGKRV 400	CC -I- SPORULATION: Toxic segment of the protein is located in the N-terminus.	
Db	358 RGGITLNNDAYINWSGHTLKYRTADSTSVTYAN-YGRITSE--KNFALEDRDIFEI 413	CC -I- SEQUENCE: 1169 AA; MW: 22EEFCFSBD699909 CRC64;	
Qy	401 YRTIANNTDVAAWPNGKVYLGVTKYDFSOYDDQNETST---YDSKRN--NCHVSAQDS 455	DR HSSP; P07130; 1DLC.	
Db	414 NSTVANL-----ANYTKAYGPGSNWTHMKRGTSSTAYLSKTHALQCTQYES 466	DR InterPro; IPR001178; Endotoxin.	
Qy	456 IDQLPPTTDEPLEKAYSHOLNYAECFLMQR----RGTIFFFTWRSVDFENTIAEK 511	DR InterPro; IPR005638; endotoxin_C.	
Db	467 SDEIPLDRT-VPVAEYSRSHLSHTSHSESKNGSAYYSFPFWTHTSADLNNTIVSDK 525	DR InterPro; IPR005639; endotoxin_N.	
Qy	61 TV---KDAVGTGIVGTGIVGRILGALGVPAQIAFYSF1VQLWPSKVDTIWBTMERVE 115	DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U04365; AA21118.1; -.	
		DR HSSP; P07130; 1DLC.	
		DR InterPro; IPR001178; Endotoxin.	
		DR InterPro; IPR005638; endotoxin_C.	
		DR InterPro; IPR005639; endotoxin_N.	
		DR InterPro; IPR008979; Gal_bind_Like.	
		DR Pfam; PF03944; Endotoxin_C; 1.	
		DR Pfam; PF00555; Endotoxin_M; 1.	
		DR Pfam; PF03945; Endotoxin_N; 1.	
		KW Sporulation; Toxin.	
		CC SEQUENCE ISOLATES;	
		DR EmbL; U043	

Qy	565 RYRVRIRYASTTNLRFVQNSNNDELVYINKTMNKDDDLTYQTF---DLATT--NSNM 618	51 ---IDPFVASTIQTGIGAKILGLTGYPPAQQASLYSFILEBLWPKGKSQMEIFMEH 107
Db	566 QYRLQRVRFASTGNPNTGKQVNLRRGGVSTIGDVRGSTNNGQELTYEEFFTRTTGPENPPF 625	114 VEVLJDKKLEYYAKSKALAELOGIQLQNNFEDVYNALNSKKTPLSLRSKRSQDRTRFLFSQ 173
Qy	619 GFSGDKNELLIIGABSFVSNEKIYDKEFIPV 650	108 VEEFINQKILTYARNKALSDLRGIGDALAVHESLWVE--NRNNTARSVYKNOYIA 164
Db	626 TFTQQEILTVNAEGVSTGGEYIIDRIEVPPV 657	174 AESHRFRNSMPSFAVSKFYLFLPTYAQANTHILLKQDQVFGEWGKSSSEDAEFTYHQ 233
RESULT 12		
C1IB_BACTB	STANDARD;	PRT; 719 AA.
ID	Q45709;	30-MAY-2000 (Rel. 39, Created)
AC		30-MAY-2000 (Rel. 39, Last sequence update)
DT		05-JUL-2004 (Rel. 44, Last annotation update)
DE	Pesticidal crystal protein cry1ib (Insecticidal delta-endotoxin Cry1 (b))	(Crystalline entomocidal protoxin) (81 kDa crystal protein).
DE	Name=cry1ib; Synonyms=cry1I(b); cryV; cryV465;	
OS	Bacillus thuringiensis "Subsp. entomocidus".	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
OX	NCBI_TaxID=14336;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SP465;	
RX	MEDLINE=953114293; PubMed=7793960;	Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;
RA	"Distribution of cry-V-type insecticidal protein genes in Bacillus thuringiensis and cloning of cry-V-type genes from Bacillus subsp. kurstaki and Bacillus thuringiensis subsp. entomocidus";	RT "Distribution of cry-V-type insecticidal protein genes in Bacillus thuringiensis and cloning of cry-V-type genes from Bacillus subsp. kurstaki and Bacillus thuringiensis subsp. entomocidus";
RT	Appl. Environ. Microbiol. 61:2402-2407 (1995).	RT
CC	-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species.	CC -I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species.
CC	CC AC On Pluteella xylosteella but not on Bombyx mori.	CC AC On Pluteella xylosteella but not on Bombyx mori.
CC	-I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC	-I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC	-I- SIMILARITY: Belongs to the delta endotoxin family.	CC -I- SIMILARITY: Belongs to the delta endotoxin family.
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DR	U07642; AAA02114.1; -	
CC	EMBL; U07642; AAA02114.1; -	
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or_send_an_email_to_licensed@isb-sib.ch).	
DR	DR HSSP; I40590; I40590.	
DR	DR InterPro; IPRO01178; Endotoxin.	
DR	DR InterPro; IPRO005638; endotoxin_C.	
DR	DR InterPro; IPRO005639; endotoxin_N.	
DR	DR InterPro; IPRO08919; Gal_bird_Ilike.	
DR	DR Pfam; PF03944; Endotoxin_C; 1.	
DR	DR Pfam; PF00555; Endotoxin_M; 1.	
DR	DR Pfam; PF03945; Endotoxin_N; 1.	
KW	KW Sporulation; Toxin.	
SQ	SEQUENCE 719 AA; 81295 MW; E8210ABAE97688E CRC64;	
Qy	1 MNPNTRNRSHTDTI-----KVTPNSELQTMHNQYPLADNPNSTEELNYKEFARMEDDS 53	Score 1124.5; DB 1; Length 719;
Db	1 MKLKNPDKHQSLSSNAVKYIATDS-----LKNTDIEILKNNNNEDYLRMSBES 50	Best Local Similarity 37.0%; Pred. No. 5.4e-65;
Qy	54 TEVDLNSTVKDAVTGTSIVGQIQIYVSVPAQALTSPYQSFLNTIWPSADPWAQMA 113	Matches 252; Conservative 135; Mismatches 229; Indels 65; Gaps 18;

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C1BC_BACTM STANDARD; PRT; 1233 AA.
 ID Q45744;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Pesticidal crystal protein cry1Bc (Insecticidal delta-endotoxin).
 DE Cry1B(c) (Crystalline entomocidal protein) (140 kDa crystal protein).
 GN Name=cry1Bc; Synonyms=cry1B(c), cry1BC;
 OS Bacillus thuringiensis (subsp. morrisoni).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=1411;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bishop, A.H.; Bone, E.J.; Ellar, D.J.;
 RT "Cloning of novel *Bacillus thuringiensis* delta-endotoxin.";
 RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
 -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
 CC epithelial cells of insects.
 CC -!- DEVELOPMENTAL_STAGE: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 CC terminus.
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.
 CC
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Z46442; CAA86568.1; -.
 DR HSSP; P02965; 1C1Y.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR InterPro; IPR008979; Gal_bind_Tk.
 PTam; PF03944; Endotoxin_C; 1.
 PFam; PF00055; Endotoxin_M; 1.
 PFam; PF03945; Endotoxin_N; 1.
 DR Sporulation; Toxin.
 KW SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;
 DR HSSP; P02965; 1C1Y.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR InterPro; IPR008979; Gal_bind_Tk.
 PTam; PF03944; Endotoxin_C; 1.
 PFam; PF00055; Endotoxin_M; 1.
 PFam; PF03945; Endotoxin_N; 1.
 DR Sporulation; Toxin.
 SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;
 Query Match 32.9%; Score 1122; DB 1; Length 1233;
 Best Local Similarity 36.7%; Pred. No. 1.7e-08; DB 1;
 Matches 247; Conservancy 126; Mismatches 248; Indels 52; Gaps 16;
 Qy 1 MNPNRNSREHDTRKTPNSBLQTHNQPLADNPNSTLEINKEFLRMTEDS---STEV 56
 Db 1 MTNSNRKNEII-----NALSIPTVSNPST---QMNLLSPDARI-BDSLCLVAYEVNN 46
 Qy 57 LDNSTVKDAGTGTGSVSGOILGVGVPPAGALTFSYQSFNLTINPSDADEPWKAQMVEV 116
 Db 47 IDEFVSAASTVQTGGINAIGRLGVQFAGQLASPFYSPFLGEIWMGRDWEIIFLVEEQ 106
 Qy 117 LIDKKIEYAKSKAIAEGLQDNNFEDYTNALNSWKTPSLRSRSKSDRIRLEFSQAES 176
 Db 107 LRQOVTNTTAAIRGLGGRRYRSQYQALETLWD--RNNDARSRSIILERYTALEL 163
 Qy 177 HFNSMSPAVSKPEVLFILPTYQAANTHILLIKDQAVFGEEMGYSSEDAYEFHQLKL 236
 Db 164 DTTAIPFLRIRNEEVPLIMVYQAANHLILLRLRDAISLSEMEWGNASSDYNQQYQOIQRY 223
 Qy 237 TQOYTDTDCVNWYANGLNGLRGSTYDAAWKENRFREMTLTVLDLIVLFFDYLRSKGV 106
 Db 224 TEYSNHCVQWNTGLNLRGTSYDAAWKENRFREMTLTVLDLIVLFFDYLRSKGVDTRTPINT 283
 Qy 297 KTELTRDIFTDP-----FSNLQTYEGPFLSIENSI-RKPHLFDLQGIBEPHT 346
 Db 284 SAQSTREITDPIGTRTAPSGFASTWNFNNAAPSSIAEEAIFPMLLDPQEQLTYS- 342

DR	Pfam; PF03445; Endotoxin_N; 1.
KW	SporeLiene; Toxin.
SEQUENCE	1215 AA; 137378 MW; 7CAFTA3311893D9B CRC64;
Qy	LQPGYFGKDSNPNWMSGNYVETRPSIGSKITITSPPFGDKSTEPVOKLSSKTFDQKVYRT 406
Qy	: : : : : : : : : : : : : : :
Db	ASSRMSSTQHMNNWYQGHRLNFRPIGTLNTNSTQGLTNTNSINPV-TLOFTSRDVRTESN 401
Qy	407 TDVAAPNGKVLYGLTVKVD-----FSQVDDQK-NETSTQTYDSKRNNGHVSQAQSIDQ 459
Db	A-----GTMILPPTPVNGVPWARENFINPQNIVYERGATTYSQVQGVQLQFDSBTTEL 454
Qy	402 A-----PPEETDEPLEKAYSHOLNAYACEFLMQDRRGTTIPFTWTHRSVDFENTIDAKITQPLPK 519
Db	455 PPEETDEPLEKAYSHOLNAYACEFLMQDRRGTTIPFTWTHRSVDFENTIDAKITQPLPK 512
Qy	460 PPEETDEPLEKAYSHOLNAYACEFLMQDRRGTTIPFTWTHRSVDFENTIDAKITQPLPK 519
Db	455 PPEETDEPLEKAYSHOLNAYACEFLMQDRRGTTIPFTWTHRSVDFENTIDAKITQPLPK 512
Qy	520 AYALSSGASLIEGGPTGGNLFLKESNSNIAKFKVTLNBSALLORYRYRASTNLR 579
Db	513 ALNLHSGTVTGGPCTGGDL-RRTNTGFGDIRLNIN-VPLSQRYRVRRASTNDLQ 570
Qy	580 LFVONSNNDPLVIVINKTMKDDDTYOTFDLATTNSNMGSQDKNEELIGAESFVSNEK 639
Db	571 FFTRINGTWNIGNFNSRTRMGRDNLEYRSRRTAGFSTPFNLAOSTFTLGAQSF-SNQE 629
Qy	640 IYDKEFFIPLQL 652
Db	630 VYIQRVEFVAEV 642
RESULT 15	
C1K4_BACTM	STANDARD;
ID	C1K4_BACTM
AC	Q45715
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Pesticidal crystal protein cryka (Insecticidal delta-endotoxin).
DE	crystal protein cryka (Insecticidal delta-endotoxin) (137 kDa crystal protein).
DB	Name=cry1Ka (Cystatine-like cry1Ka; cry1K(a)).
GN	Bacillus thuringiensis (Subsp. morrisoni).
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC	NCBI_TaxID=1441;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	MEDLINE-96102856; PubMed=8588263; DOI=10.1016/0378-1097(95)00397-1;
RX	Koo B.T., Park S.-H., Choi S.-K., Shin B.-S., Kim J.-I., Yu J.H.;
RA	"Cloning of a novel crystal protein gene cry1K from Bacillus thuringiensis subsp. morrisoni."
RT	FEMS Microbiol. Lett. 134:155-164 (1995).
RL	- FUNCTION: Promotes colloidosomatic lysis by binding to the midgut epithelial cells of insects. Selectively toxic to <i>Artoeia rapae</i> but not active on <i>Pluteola xylosteala</i> .
CC	- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC	- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC	- SIMILARITY: Belongs to the delta endotoxin family.
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CC	RESULT 16
C7AA_BACTU	STANDARD;
ID	C7AA_BACTU
AC	Q03719;
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Pesticidal crystal protein cry7Aa (Insecticidal delta-endotoxin Cry7Aa) (Cystatine entomocida protein) (129 kDa crystal protein).
DB	Synonyms=cry7IIC, cry7IA(a);
DR	Name=cry7Aa; Sequence7aa.
DR	NCBI Name=cry7Aa.
DR	Bacilli Thuringiensis.
DR	OC
DR	NCBI_TaxID=1423;
DR	SEQUENCE FROM N.A.
DR	RP

RX MEDLINE=92384571; PubMed=1514800;	Qy 467 PLEKAYSHOLNVAECFCIMQD---RRCTTIPFFTWRHSVDPFFNTIDAEEKITOLPVVYKAYL 523
PA Lambot B.; Hotte H.; Annys K.; Jansens S.; Soetaert P.; Peferoen M.;	Db 449 PIHEKYTHRLCHATAIFKSTPDDNTATPSWTHSAEYNRIPNKTKIPAVKYL 508
RT "Novel Bacillus Thuringiensis insecticidal crystal protein with a silent activity against coleopteran larvae.";	
RL Appl. Environ. Microbiol. 58:2536-2542(1992);	
CC -!- FUNCTION: Promotes cellular lysis by binding to the midgut epithelial cells of Coleoptera. This protein is not toxic in its natural form. It is highly toxic to Colorado potato beetle larvae after an in vitro solubilization and trypsin activation step.	Qy 524 SSASATIEGPGBTGCGNLFLKESSNSIAKPTVLTNSAALLQRYRVRVYATNNRIPKTYIPAVKYL 583
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	Db 509 DBPSTVKPGTGGDLY-KRSTGTVGIDIKATVNS_PLSQKRYRVRVYAT----- 557
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	Qy 584 NSNNDFLVYIN-----KMNKDDDLTYQFDLATTNSMGFSGCDKNEIIG 630
CC -!- SIMILARITY: Belongs to the delta endotoxin family.	Db 558 NVSGQFNV-YINDKLTQTKFQNTVERIGEGRDTIGSFGTYEYSTTQFDEHPKTLH 616
CC -----	Qy 631 AESFSVNEKVIYDKEIPTPVOL 652
CC -----	Db 617 LSDLSNNSFYVDSIEFIPVDV 638
CC -----	Qy 617 Q9FPB8 PRELIMINARY; PRT; 719 AA.
CC -----	Db 617 Q9FPB8 PRELIMINARY; PRT; 719 AA.
RESULT 17	
CC -----	Q9FPB8 PRELIMINARY; PRT; 719 AA.
CC -----	AC Q9FPB8; Created) (TREMBrel. 16, Last sequence update)
CC -----	DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)
CC -----	DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
DR EMBL; M64478; AAA22351_1; -.	DR RN Sequence from N.A.
DR EMBL; A07236; CAR0646_1; -.	DR OS Strain and characterization of a novel cryII-type gene. n.
DR PIR: A48944; A48944.	DR OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus thuringiensis.
DR HSSP; P07130; IDIC.	DR NCBI_TaxID:1428;
DR InterPro; IPR001178; Endotoxin.	DR RN Sequence from N.A.
DR InterPro; IPR005638; endotoxin_c.	DR RC STRAIN=BTC007;
DR InterPro; IPR005639; endotoxin_N.	DR RX MEDLINE=22837682; PubMed=12957903;
DR InterPro; IPR008979; Gal-bind_Iike.	DR RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J., Li G., Huang D., Hu Y., Li G., Huang D., RT "Identification of cryII-type genes from Bacillus thuringiensis strains and characterization of a novel cryII-type gene. n."
DR Pfam; PF03944; Endotoxin_C; 1.	DR DR DOI=10.1128/AM.69.9.5207-5211.2003;
DR Pfam; PF00555; Endotoxin_M; 1.	DR DR IntePro; IPR005638; endotoxin_C.
DR Pfam; PF03945; Endotoxin_N; 1.	DR DR IntePro; IPR005639; endotoxin_N.
KW Sporulation; Toxin.	DR DR IntePro; IPR008979; Gal_bind_Iike.
SEQUENCE 1138 AA; 129391 MW; 69DB676D4F6A1FAC CRC64;	DR DR Pfam; PF00944; Endotoxin_C; 1.
Best Local Similarity 32.9%; Score 1119; DB 1; Length 1138; Matches 251; Conservative 120; Mismatches 237; Indels 74; Gaps 19;	DR DR Pfam; PF00555; Endotoxin_M; 1.
Matches 251; Conservative 120; Mismatches 237; Indels 74; Gaps 19;	DR DR Pfam; PF03945; Endotoxin_N; 1.
Db 1 MNPNRNSEDTDITKVTPNSELQTNHQNQYPLADNPNSTELBNYKEPLMTEDSSTEVLDS 60	KW Plasmid.
Db 1 MNLRNLDGSEDTNSPTLNSL----NYTQKALSPSKNMNQYDLSITSETEPEALAGS 55	SEQUENCE 719 AA; 81024 MW; 7E17481922C43B6 CRC64;
Qy 1 MNPNRNSEDTDITKVTPNSELQTNHQNQYPLADNPNSTELBNYKEPLMTEDSSTEVLDS 60	Query Match 32.8%; Score 1118.5%; DB 2; Length 719;
Qy 1 MNLRNLDGSEDTNSPTLNSL----NYTQKALSPSKNMNQYDLSITSETEPEALAGS 55	Best Local Similarity 37.3%; Pred. No. 1.3e-64; Mismatches 235; Indels 61; Gaps 17;
Qy 61 TVKDAVGTRGTSVWQIQLGVGVPFAGALTFSYQFLNTIWPSPADPKAFMAQEVNLIDK 120	Db 1 MNPNNNSEHDAT-----KVTPNSELQTNHNOYPLADNPNSTLBEILNYKEPLMTEDSS 53
Qy 61 TVKDAVGTRGTSVWQIQLGVGVPFAGALTFSYQFLNTIWPSPADPKAFMAQEVNLIDK 120	Db 1 MKLNKNDPKHOSSLSSNAKVDKIATDS-----LNRTDIELKNINHEDFLRMSEHES 50
Db 56 NT--AINTVSVTGTLSALGVPAFSITNFVYKIALGLWPENGKINDEFTEVEALIDQ 113	Qy 1 MNPNRNSEDTDITKVTPNSELQTNHQNQYPLADNPNSTELBNYKEPLMTEDSS 53
Db 112 KIEEYAKSKAKAAELGQDNQFEDYNALNSW---KKTPSLRSRSKRSODIRELFSQAESH 177	Db 54 TEVLDSLNTVKDAVGTRGTSVWQIQLGVGVPFAGALTFSYQFLNTIWPSPADPKAFMAQ 113
Db 114 KIEEYVRNKAIAEGLGSLSDKQKALDWLGKQDDPPEAISVATEPRI----IDS 167	Db 55 1 IDPFEVSYTQGIGIAKSLGTLGVPPFAGQASLSSPFLGKERSQWLFMEH 107
Qy 178 FRNSMSPAVSKPEVTFELPTYAQOANTHLLKLKDAAQVFGEWGSSEDVAEPYHROLKT 237	Qy 1 114 VEVLDKRIEEYAKSKAKAAELGQDNQFEDYNALNSWKKTPSLRSRSKRSODIRELFSQ 173
Db 168 FEFSMSPAVSKPEVTFELPTYAQOANTHLLKLKDAAQVFGEWGSSEDVAEPYHROLKT 227	Db 1 1 MLKLNKNDPKHOSSLSSNAKVDKIATDS-----LNRTDIELKNINHEDFLRMSEHES 50
Db 238 QQYDHICWVNYNGLNGRLGSTYDAWKENRFRREMILTLVLFPPDYIRLYSKGVK 297	Qy 1 TQLTREVVYDPEVSLISNPDIGPSQSMENTAIRTPHLADYDLEYITTSKYKAFSHBLQ 347
Db 228 SEYSDHCTKWNGLSRLNGSTYEQWINNQRFRREMILMALDVLAVFPHDPYRYSMETS 287	Db 1 108 VEEILDQISTYARNIAALDKLGGLDALAYTHELESWIK--NTRNARATSWKSQYIA 164
Qy 298 TELTRDIFTDPIFSLNTLQDQYGPFTLISI-SIRKPHLFDYLOGIEHT-----RLQ 348	Qy 1 109 VEEILDQISTYARNIAALDKLGGLDALAYTHELESWIK--NTRNARATSWKSQYIA 164
Db 288 TQLTREVVYDPEVSLISNPDIGPSQSMENTAIRTPHLADYDLEYITTSKYKAFSHBLQ 347	Db 1 109 VEEILDQISTYARNIAALDKLGGLDALAYTHELESWIK--NTRNARATSWKSQYIA 164
Qy 349 PGYFGKDFSENWSGNVYETRPSIGSSKTTISPFYGDKSTPVEKQ---LSDPGQKVERTIAN 406	Qy 1 110 VEEILDQISTYARNIAALDKLGGLDALAYTHELESWIK--NTRNARATSWKSQYIA 164
Db 348 PDLF-----TWSAHKVPSFKGS-EOSNLNTTIGING-KTSGYISSGAYSHGNDIVRTLA 399	Db 1 110 VEEILDQISTYARNIAALDKLGGLDALAYTHELESWIK--NTRNARATSWKSQYIA 164
Qy 407 TDVAAMPNGKTYQYLGTVKVDQSYYDQQKNETSOTYDSKRKNNGHVSQDSDOLPPETDE 466	Db 1 111 VEEILDQISTYARNIAALDKLGGLDALAYTHELESWIK--NTRNARATSWKSQYIA 164
Qy 400 PSVWVVPYQNY-GVEQVFYGVKGHVVHRDQKNDK-----LTYPSIDQLPPD--GE 448	Qy 1 112 VEEILDQISTYARNIAALDKLGGLDALAYTHELESWIK--NTRNARATSWKSQYIA 164
Db -----	Db 1 113 VEEILDQISTYARNIAALDKLGGLDALAYTHELESWIK--NTRNARATSWKSQYIA 164

DE	Pesticidal crystal protein cryIIId (Insecticidal delta-endotoxin (81 kDa crystal protein).
DE	Name=cryIIId; Synonyms=cryIIId; Rho; NhcryV;
GN	Bacillus thuringiensis
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC	
OX	NCBI_TaxID=1428;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BR30;
RA	Medline=20374042; PubMed=10919402;
RT	Choi S.-K.; Shin B-S.; Kong E.-M.; Rho H.M.; Park S.-H.;
RT	"Cloning of a new <i>Bacillus thuringiensis</i> cryIIId-type crystal protein gene."
RL	Curr. Microbiol. 41:65-69(2000).
CC	-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae. Active on <i>Plutella xylostella</i> and on <i>Bombyx mori</i> .
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.
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DR	EMBL; AF041579; ADD41366.1; -.
DR	HSSP; P02965; ICIYI; Endotoxin.
DR	InterPro; IPR001178; Endotoxin.
DR	InterPro; IPR005638; endotoxin_C.
DR	InterPro; IPR005639; endotoxin_N.
DR	InterPro; IPR008379; Gal_bind_like.
DR	Pfam; PF03944; Endotoxin_C_1.
DR	Pfam; PF00555; Endotoxin_M_1.
DR	Pfam; PF03945; Endotoxin_N_1.
KW	Sporulation; Toxin.
SQ	SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;
Qy	Query Match 32.8%; Score 1115.5; DB 1; Length 719; Best Local Similarity 37.8%; Pred. No 2, 1e-64; Matches 253; Conservative 123; Mismatches 225; Indels 69; Gaps 18;
Db	5 NONMYRSPSSNATVDKSFTDPLEHTNMLQNHNEDGLKNSBEYESVPFVSVTQ--- 61
Qy	67 GTGIVSVGGILGVGVPPAGALTSPYQSFNLNTWDADPKAFMAQEVLIDKKIEEYA 126
Db	62 -TGIGIAKGILGNIGVPPAGQVASLYSTFLGELWPKGSKQWLFMEVLLINQKISTYA 120
Qy	127 KSKKALAEIQLGQNPFEDVNAIWNWKTPLSRSRSRDRIBEL---FSQAEBSHFRNSM 182
Db	121 RNKALADLGKGDAIATVHSLSWIE----NRNTRVRSVVKNOYIALEMFWYQKL 173
Qy	183 PSFAVSKKEFYFLPFTYAOAANTHLLKKAQVFGEECYSSSEDAEYHROKLTKQQYTD 242
Db	174 PSFAVSGEVPLPFTYAOAANHLLRASIGKEWGISESISTFNRSQSQTQEYSD 233
DR	EMBL; U04167; AAA21120.1; -.
DR	HSSP; P07130; IDLC.
DR	InterPro; IPR001178; Endotoxin.
DR	InterPro; IPR005638; endotoxin_C.
DR	InterPro; IPR005639; endotoxin_N.
DR	InterPro; IPR008379; Gal_bind_Like.
DR	Pfam; PF03944; Endotoxin_C_1.
DR	Pfam; PF00555; Endotoxin_M_1.
DR	Pfam; PF03945; Endotoxin_N_1.
KW	Sporulation; Toxin.
SQ	SEQUENCE 1138 AA; 129778 MW; 01DF7072C07CE88 CRC64;

Query Match Score 32.6%; Score 1112; DB 1; Length 1138;
 Best Local Similarity 36.8%; Pred. No. 6..8-64;
 Matches 248; Conservative 124; Mismatches 244; Indels 58; Gaps 19;

Qy 1 MNPNRSEHDITKTPNSLQTNHQYPLADNPNSTLEELNRYKREFRMEDSSTEVLDS 60
 Db 1 MNLNLLGGYEDDSNRNLNSL---NYPTOKALSPSLNNYYQDFLSITREQPEALASG 55
 Qy 61 TVKDAVGTGIVSGVQTLGVGVPPFGALSFSYOSPLNTWPSDAPMKFMAQEVEVLDK 120
 Db 56 NT--AINTTYSVTGATLSLQWGFATNMFYLKITLGWPHNKNWIDFMTETVETLIEQ 113
 Qy 121 KIEEYAKSKALAELOGLQNNEFDYINALLSWKTKPLSLRSKRSODRIRLFQSQAEHFFN 180
 Db 114 KIEQFARNKALAELEGGLGNLTITQQALEDWNNP--DDPATITRVIRFRFLDLPES 170
 Qy 181 SMPFAVSKEFVLPETYAQANTHLLLRDAQVFGEENGYSSSDVAEFYHROLKLTOCY 240
 Db 171 YMPSPRVAEGEPIPLTVYAQANHLALLDRSTLYGDKGWFTQNNEENYNRQCKHISSE 230
 Qy 241 TDHCYCNWYNGVNLGLRGYSTDAWYKFNRFEREMTILTVLILIVLFFYDRLYSKGVKTDL 300
 Db 231 SNHCVKRWNGSLRSLNGSTEQWQNWYNREREMTILMVLDIAAVPYDPRMYSMETSQL 290
 Qy 301 TRDIFTDPISLNLTLQEKYGPFTFLSEN-STRKPHLFDTQGIEPHT-----RLQGY 351
 Db 291 TREVYTDPLSLSNPDIGSFSGMENTAFRTPLHVDYLDELYIYTSKYKAFSHIEQDPL 350
 Qy 352 FGKDSFNYNGNYVETRSPSIGSSKTTSFYGDKSTEPVQK--LSFDGCKVYRTIANTDV 409
 Db 351 F----YNCVHKYSPFKKS-EQSNLYTTGTYG-KTSGYISSGAYSFRGRNDIYRTLAAPS 402
 Qy 410 AAWPNGKVYLVGTYKWDFSQYDQKNETSTQTYDSEKRKNNGHVSAQDSTQDOLPPETDPEL 469
 Db 403 VVYPTQNTY-GVEQVEFYGVKGYHYGRNQKYD-----LTYDSIDLQPPD--GEPTH 451
 Qy 470 KAYSHOLNAYAECFLMQD---RRGTTIPPFWTHRSYDFPNTIDAKitQPVVKAYAISG 526
 Db 452 EKYTHRCHATAISKSTPQDYNATPIFISSWTHRAEYNNRIPNPKIKIPAVKMYKLDDL 511
 Qy 527 ASIIEPGGTTGGNLLFLKRESSNS-TAKEFVTLNSAALQYRYRIRYASTTN--LRLFVQ 583
 Db 512 STVVKGPGFGGDL -VRKGSGNGYIGDIKATNS -PLSSKYYRVRVATSVSGLFNVFI - 567
 Qy 584 NSNNDFLYIN-----KTMNKDDQDLYCTCFDLATTNSMGFSGDKNLLIGAESFVNE 638
 Db 568 ---NDEIAIQKNFQSTVETIGEGRDLYTGSFGYIEYSTTQFPNHEPKTILHNLSNNS 624
 Qy 639 KIYDKEFIPVQL 652
 Db 625 PFYVDSIETIPVVD 638

RESULT 21

C1A_BACTK STANDARD; PRT; 719 AA.
 ID_C1A_BACTK
 AC Q45752; P71052; Q45751; Q45756;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Pesticidal crystal protein cry1a (Insecticidal delta-endotoxin
 DB CRY1 (a)) (Crystalline entomocidal Protein) (81 kDa crystal protein).
 OS Bacillus thuringiensis (subsp. kurstaki).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=29339;
 RP SEQUENCE FROM N.A.

STRAIN=DSIR732;
 MEDLINE=93298009; PubMed=8517758;
 Gleave A.P., Williams R., Hedges R.J.;
 "Screening by polymerase chain reaction of *Bacillus thuringiensis*"

KW Sporulation; Toxin; Variant 159 K -> R (in strain 61).

PT	VARIANT	233	233	D -> Y (in strain JHCC4835 and strain HD-1).	RA	Song F., Zhang J., Gu A., Huang D., Li G.; submitted (APR-2001); EMBL/GenBank/DBJ databases.
PT	VARIANT	443	443	A -> V (in strain AB98).	DR	AF573207; AF5965; 1.CY.
PT	VARIANT	711	712	KQ -> NE (in strain HD-1 and strain 61).	DR	HSSP; P09965; 1.CY.
SEQUENCE	SEQUENCE	719 AA;	81216 MW;	3627E5A6C25DAFF5 CRC64;	DR	GO: GO:0005102; F: receptor binding; IBA.
Query Match	Best Local Similarity	32.3%	Score	1100.5; DB 1; Length 719;	DR	GO: GO:0006952; P: defense response; IBA.
Matches	249	Conservative	137;	Mismatches 231; Indels 63; Gaps 19;	DR	GO: GO:000905; P: pathogenesis; IBA.
Qy	1	MNPNNRSEHDFTI-----KVTPNSELQTNEINQYPLADPNSTLEELNYKEFLRMTEDSS 53	DR	InterPro; IPR001175; Endotoxin C.		
Db	1	MKLKNQDQKHQSFSNAVKD1KSTDs-----LKNEDEIOLINHBCUCLMSEYEN 50	DR	InterPro; IPR005638; endotoxin N.		
Qy	54	TE-VLDNSTVDAVTCGISVQILGVGVPGAGALTSEYFVNALNSWKTPLSLRSKSQDRRELFS 112	DR	InterPro; IPR005639; endotoxin N.		
Db	51	VEPFVSASTIQ---TGIGIACKLGLTGPVAGQASLYSFILGPWLWPKCKNQWEIFME 106	DR	InterPro; IPR008979; Gal bind Like.		
Qy	113	QVEVLIDKKIEPYAKSKAALAEQLQGLONNFEDYVNALNWSWKTPLSLRSKSQDRRELFS 172	DR	Pfam: PF03944; Endotoxin C; 1.		
Db	164	ALBLMFVTKQLPSFAVSCEEVPLPLPITAQANHLILLRDASIFGEKGWLSSSEISTFYNR 223	DR	Pfam: PF00555; Endotoxin M; 1.		
Qy	233	QKLQTQYTDHCYVNWVNGVNLGLRGSTSYDAVWKENPERRENTLVLDLTVLFPPFDIRLY 292	DR	Pfam: PF03945; Endotoxin N; 1.		
Db	224	QAESHFRRNSNMPFAVSKPEVFLPLTYAQAAANTHLLIKDAAVGFEGWYSSVEDAEFYHR 232	DR	SEQUENCE 719 AA; MW: C629DFC44827241 CRC64;		
Qy	173	TAESHFRRNSNMPFAVSKPEVFLPLTYAQAAANTHLLIKDAAVGFEGWYSSVEDAEFYHR 232	Qy	1 MNPNRSEHDFTI-----KVTPNSELQTNEINQYPLADPNSTLEELNYKEFLRMTEDSS 53		
Db	164	ALBLMFVTKQLPSFAVSCEEVPLPLPITAQANHLILLRDASIFGEKGWLSSSEISTFYNR 223	Qy	1 MNLKNQDQKHQSFSNAVKD1KSTDs-----LKNEDEIOLINHBCUCLMSEYEN 50		
Qy	233	QKLQTQYTDHCYVNWVNGVNLGLRGSTSYDAVWKENPERRENTLVLDLTVLFPPFDIRLY 292	Qy	1 MNLKNQDQKHQSFSNAVKD1KSTDs-----LKNEDEIOLINHBCUCLMSEYEN 50		
Db	224	QERAGDYSDHCVKYSTGMLNLRGTAEAWSVRYNQFRDTMLVLDLVALFPSTDTQMV 283	Qy	54 TE-VLDNSTVDAVTCGISVQILGVGVPGAGALTSEYFVNALNSWKTPLSLRSKSQDRRELFS 172		
Qy	293	SKGVKTBELTRDIFTD-----PIFSLNT-LQEYQPTPELIENS-IRKPHILEDYLQGIE 342	Db	51 VEPPFVSASTIQ---TGIGIACKLGLTGPVAGQASLYSFILGPWLWPKCKNQWEIFME 106		
Db	284	PIKTTAQALIREVYTDAIGVWHHPSPFSTTMWYNNNAFSEALEAAYVNRNPLLDFLEQVT 343	Qy	113 QVEVLIDKKIEPYAKSKAALAEQLQGLONNFEDYVNALNWSWKTPLSLRSKSQDRRELFS 172		
Qy	343	FHTRLQPGYFGKDSFNTVGNWGNVETRPSIGSSRTITSFVXDKSSTEPVQKLISFDQKVR 402	Db	107 HVEE1NQKLSITYAENKALTDLGIGDALAVYHISLESWVG--NRNNTTRARSVYKSQYI 163		
Db	344	IYSSLR-RWSNTQYMMNMWGHKLEFR-TIGGTLNINSTQQNTNTSINPV-TLPFTSRDVYR 400	Qy	173 QAESHFRRNSNMPFAVSKPEVFLPLTYAQAAANTHLLIKDAAVGFEGWYSSVEDAEFYHR 232		
Qy	403	TIANTDVAAWPNQKVKYLVGTVKDFQDDQNETSTOTYDSKRNNGH---VSAOPSDQ 458	Db	164 ALBLMFVTKQLPSFAVSCEEVPLPLPITAQANHLILLRDASIFGEKGWLSSSEISTFYNR 223		
Db	401	TESLAGINLFLTQPVN-GVPRDF---HWKFVTHPLASDNFYYPGAGTQLQDSEN 455	Qy	233 QKLQTQYTDHCYVNWVNGVNLGLRGSTSYDAWVKENPERRENTLVLDLTVLFPPFDIRLY 292		
Qy	459	LPPETTDEPLEKAYSHOLNAYABCFELMQDRGRTIPFFTWTHRSVDFENTDAEKITQLPVY 518	Db	224 PFKTTAQALIREVYTDAIGVWHHPSPFSTTMWYNNNAFSEALEAAYVNRNPLLDFLEQVT 343		
Db	456	LPPEATCOPTEYSYSHRLSHIGHLISASHVKAHV-YSWTHRSADRNTTNPNSITOPLY 513	Qy	293 SKGVKTBELTRDIFTD-----PIFSLNT-LQEYQPTPELIENS-IRKPHILEDYLQGIE 342		
Qy	519	KAYALSSGAS11BGPGBTGQNLLFLKESNSNIAKFTVTLNSAALLORYRIRYASTTNL 578	Db	284 PIKTTAQALIREVYTDAIGVWHHPSPFSTTMWYNNNAFSEALEAAYVNRNPLLDFLEQVT 343		
Db	514	KAFNLSSGAAVVRGPGBTGQDFDL-RTNTNGTGFDIRVNIN-PPFAQRYRIRYASTTDL 571	Qy	343 FHTRLQPGYFGKDSFNTVGNWGNVETRPSIGSSRTITSFVXDKSSTEPVQKLISFDQKVR 402		
Qy	579	RLFVQ----NSNNDFLFLVYINKTMKDDDLTYQFDLATTNSNGFSGDRKNELLIGAE 632	Db	344 IYSSLR-RWSNTQYMMNMWGHKLEFR-TIGGTLNINSTQQNTNTSINPV-TLPFTSRDVYR 400		
Db	572	QFHTSINGKAINQGN----FSATMNRGDEDLYKTFRTVGETTPFSFLDVQSTFTIGAN 625	Qy	403 TIANTDVAAWPNQKVKYLVGTVKDFQDDQNETSTOTYDSKRNNGH---VSAOPSDQ 458		
Qy	633	SFVSNEKUYIDKIEFIPVQL 652	Db	401 TESLAGINLFLTQPVN-GVPRDF---HWKFVTHPLASDNFYYPGAGTQLQDSEN 455		
Db	626	NFSSGNENVYDREFEVVE 645	Qy	459 LPPETTDEPLEKAYSHOLNAYAECFLMDQRGRTIPFFTWTHRSVDFENTDAEKITQLPVY 518		
RESULT 22	Q93NJ5	PRELIMINARY;	Db	514 KAFNLSSGAAVVRGPGBTGQDFDL-RTNTNGTGFDIRVNIN-PPFAQRYRIRYASTTDL 571		
ID	Q93NJ5;	PRT;	579 RLFWQ----NSNNDFLFLVYINKTMKDDDLTYQFDLATTNSNGFSGDRKNELLIGAE 632			
AC	Q93NJ5;	719 AA.	572 QFHTSINGKAINQGN----FSATMNRGDEDLYKTFRTVGETTPFSFLDVQSTFTIGAN 625			
DT	01-DEC-2001	(TREMBLrel. 19, Created)	633 SFVSNEKUYIDKIEFIPVQL 652			
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	626 NFSSGNENVYDREFEVVE 645			
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)	NAME=CRY11a.			
DE			Bacillus thuringiensis.			
GN			Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OS			NAME=CRY11a.			
OC			NCBI_TaxID:1428;			
OX			[1]			
RN			SEQUENCE FROM N.A.			
RP						

DT	05-JUL-2004	(TREMBLrel. 27, Created)	Qy	633 SFVSNKEKIVIDKIEFIPVQL 652
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)	Db	626 NFGSGNEVYDRIEVPVVEV 645
DE	CryII.			
GN	Bacillus thuringiensis	RESULT 24		
NCBI_TaxID	1428;	Q8K761	PRELIMINARY;	PRT, 719 AA.
RN	[1]	ID Q8K761;		
RP	SEQUENCE FROM N.A.	AC Q8K761;		
RA	Espindola R., Lemos M.V.P., Lemos B.G.M., Sena J.A.D.; Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.	DT 01-OCT-2002 (TREMBLrel. 22, Created)		
RL	EMBL:AY62167; AAP86782.1; -	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)		
DR	GO:000102; F:receptor binding; IEA.	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DR	GO:0006952; P:defense response; IEA.	OS Bacillus thuringiensis.		
DR	PFam: PF009405; P:pathogenesis; IEA.	OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; NCBI_TaxID=1428;		
DR	InterPro: IPR001178; Endotoxin.	OX DR GO; GO:0005102; F:receptor binding; IEA.		
DR	InterPro: IPR005638; endotoxin_C.	DR GO; GO:0006932; P:defense response; IEA.		
DR	InterPro: IPR005639; endotoxin_N.	DR InterPro; IPR001178; Endotoxin.		
DR	InterPro: IPR0086979; Gal_bind_Like.	DR InterPro; IPR008979; Gal_bind_Like.		
DR	Pfam: PF03944; Endotoxin_C; 1.	DR Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam: PF01945; Endotoxin_N; 1.	DR Pfam; PF01945; Endotoxin_N; 1.		
SQ	SEQUENCE 719 AA; 81216 MW;	3627E5A6C25DAFF5	CRC64;	SEQUENCE 719 AA; 80984 MW;
Qy	Query Match Score 1100.5; Pred. No. 2e-63; Length 719; Best Local Similarity 36.6%; Matches 249; Conservative 137; Mismatches 231; Indels 63; Gaps 19;	Query Match Score 1096.5; Pred. No. 3.7e-63; Best Local Similarity 36.2%; Mismatches 246; Conservative 142; Mismatches 229; Indels 63; Gaps 18;		
Db	1 MNPNRSEHDITI-----KVTPNSELQTNHNOYPLADNPNSTLBELNYKEFLRMTEDS 53	Qy 1 MNPNRSEHDITI-----KVTPNSELQTNHNOYPLADNPNSTLBELNYKEFLRMTEDS 53		
Qy	1 MKLNQDQHOSPFSSNAVKDKISTDS-----LKNETDIELQNINHBDCLRMSEYEN 50	Db 1 MKLNQDQHOSPFSSNAVKDKISTDS-----LKNETDIELQNINHBDCLRMSEYEN 50		
Qy	54 TE-VLDNSTVKAQVTDGIGSVQGLGVVCPPEAGALTYSQSFLNTINWSDAPWKAFM 112	Qy 54 TE-VLDNSTVKAQVTDGIGSVQGLGVVCPPEAGALTYSQSFLNTINWSDAPWKAFM 112		
Db	51 VEPPVASTIQ---TGIGIAKGKLTGTVPEAGQVASYLSPEFLGELWPKGNQWEIME 106	Db 51 VEPPVASTIQ---TGIGIAKGKLTGTVPEAGQVASYLSPEFLGELWPKGNQWEIME 106		
Qy	113 QVEVLIDKIEEYAKSKALAELOGLQNNFEDYNALNSRKTPUSLRSRSQRIRELTS 172	Qy 113 QVEVLIDKIEEYAKSKALAELOGLQNNFEDYNALNSRKTPUSLRSRSQRIRELTS 172		
Db	107 HVEEINQKISTYARNKALTDLKGIGDALAVYHOSLESWVG--NRNTRNTRASVTKSQYI 163	Db 107 HVEEINQKISTYARNKALTDLKGIGDALAVYHOSLESWVG--NRNTRNTRASVTKSQYI 163		
Qy	173 QAESHFRNNSMPSFAVKSKFEYLFLPTYAQAQANTHLLLKDQVPGEEWGSSEDVAEFYHR 232	Qy 173 QAESHFRNNSMPSFAVKSKFEYLFLPTYAQAQANTHLLLKDQVPGEEWGSSEDVAEFYHR 232		
Db	164 ALELMFVQKLPSFAVSGEEVPLPYIQAQANLHLRLRASIFGEWGLISSEBTIFN 223	Db 164 ALELMFVQKLPSFAVSGEEVPLPYIQAQANLHLRLRASIFGEWGLISSEBTIFN 223		
Qy	233 QKLUTQQYTDHCYWNWYNGLNGLRGSTDYDAWKENFREMTLTVDLIVLFYDIRLY 292	Qy 233 QKLUTQQYTDHCYWNWYNGLNGLRGSTDYDAWKENFREMTLTVDLIVLFYDIRLY 292		
Db	224 QVERZAGDWSWRVYQNFREDMTMVLQDVALFPSYDTQMY 283	Db 224 QVERZAGDWSWRVYQNFREDMTMVLQDVALFPSYDTQMY 283		
Qy	293 SKGVKTELLRDIFD-----PIFSLNT-LQEYGPFLSLENS-IRKPHLDYLOGIE 342	Qy 293 SKGVKTELLRDIFD-----PIFSLNT-LQEYGPFLSLENS-IRKPHLDYLOGIE 342		
Db	284 PIKTTAQLTREVYTDAIGTVHPHESFTSTWYNNNAPSSAIAAVVRNPHLDFLEQVT 343	Db 284 PIKTTAQLTREVYTDAIGTVHPHESFTSTWYNNNAPSSAIAAVVRNPHLDFLEQVT 343		
Qy	343 FHTRLQPGFPGKDSFNYWGNVNGLNGRSTYDAWKENFREMTLTVDLIVLFYDIRLY 292	Qy 343 FHTRLQPGFPGKDSFNYWGNVNGLNGRSTYDAWKENFREMTLTVDLIVLFYDIRLY 292		
Db	344 IYSLSL-RWSNTQYMMWGHKLER-TIGGTININSTQSTSNTSINPY-TLPPTSRDYR 400	Db 344 IYSLSL-RWSNTQYMMWGHKLER-TIGGTININSTQSTSNTSINPY-TLPPTSRDYR 400		
Qy	403 TIANTDVAAPNGKVKLGYTKVDPQYDQKNETSTOTYDSKRNGH---VSAQDSIDQ 458	Qy 403 TIANTDVAAPNGKVKLGYTKVDPQYDQKNETSTOTYDSKRNGH---VSAQDSIDQ 458		
Db	401 TESLAGLNFLTQPVN-GPVRVDF----HMKWFTHPIASDNFTYPGYAGIGTQLODSEN 455	Db 401 TESLAGLNFLTQPVN-GPVRVDF----HMKWFTHPIASDNFTYPGYAGIGTQLODSEN 455		
Qy	459 LPPETTDEPLEKAYSHQMLYABCFLMDQDERGTIPPFWTWRSYDFFNTIDAEKITOLPV 518	Qy 459 LPPETTDEPLEKAYSHQMLYABCFLMDQDERGTIPPFWTWRSYDFFNTIDAEKITOLPV 518		
Db	456 LPPEATGQNYESTSHRLSHIGLTSASHVTKALV--YSWTHRSADRNTTEPEPSITQ1PV 513	Db 456 LPPEATGQNYESTSHRLSHIGLTSASHVTKALV--YSWTHRSADRNTTEPEPSITQ1PV 513		
Qy	519 KAYLSSGASLIEGGFTGNLFLKLESSNSIAKFKTILNSAALLQRYRIRYASTTNL 578	Qy 519 KAYLSSGASLIEGGFTGNLFLKLESSNSIAKFKTILNSAALLQRYRIRYASTTNL 578		
Db	514 KAFNLSSGAAVVRGPFTGFDIL-RRTNTGFTGDIRVNTN-PPFAQRYRIRYASTDL 571	Db 514 KAFNLSSGAAVVRGPFTGFDIL-RRTNTGFTGDIRVNTN-PPFAQRYRIRYASTDL 571		
Qy	579 RLRFQ----NSNNDFLVYIYNTMNKKDDLYQTFDIAATTNSNMGSGDKNELIGAE 632	Qy 579 RLRFQ----NSNNDFLVYIYNTMNKKDDLYQTFDIAATTNSNMGSGDKNELIGAE 632		
Db	572 QFHTSINGRAINQGN-----FSATMNRGBDLDYKTFRTVGFITPFSFLDVQSTFTGAW 625	Db 572 QFHTSINGRAINQGN-----FSATMNRGBDLDYKTFRTVGFITPFSFLDVQSTFTGAW 625		
Qy	639 LPPETDDEPLEKAYSHOLNYAECFLM2DRRGTFPEFTWHSYDFNTIDAEEKITOLPVV 518	Qy 639 LPPETDDEPLEKAYSHOLNYAECFLM2DRRGTFPEFTWHSYDFNTIDAEEKITOLPVV 518		

Db	456	LPPETGQPNYESYSHRLSHIGLISASHVKALV-- YSWTHRSADRTNTIBPNSITQIPLV	513	Db	284	PIKTTAQLTREVTYDAIGTVPHPHSFSTSTWYNNAAPSSAIEAVRNPHLLDFLEQVT	343
Qy	519	KAYALSGGASLIEGPGTGTGNNLFLKKESSNSIAKEFVTLNSAIIQLQYRIRYASTNII	578	Qy	343	FHTRLQPGYFGKDSNYWGNVYTRPSIGSSKTTISPFYGDKSTEPIQKLSPDGQKYR	402
Qy	514	KAFNLSSGAIVVRGPGTGGDL-L-RCTNTGTFGDLRVNIN_PPFQARYRIRYASTTDDI	571	Db	344	IYSLIS-RWSNTQMMWGGHKLFR-TIGGLUNISTQGSTNTNVP-TLPFTSRDVYR	400
Qy	579	RLFVQ----NSNNNDFLVYIINKTKNKKDDDTYQEDPLATTSNSNGFSQDRNLIGAE	632	Qy	403	TIANTDVAAMPNGKVYLGTVKDFSQYDDQKNETSTQYDSKRANGH---VSQDSDIQ	458
Db	572	QPHTSINGKANQGN----FSATMNRGEQEDLYDKTPRTFPTPSFVQSTFTIGM	625	Qy	459	LPPETTDEPLEKAYSHOLQNAECFLMDQRGTTIPFFTWTRSYDFENTIDAEEKITQLPVV	518
Qy	633	SFVSNEKLYIDKIEFIPVQL	652	Qy	459	401 TESLAGLNELTQPN-GIVPRVDF -- -HWKFVTHPIASDMNPYFYGIGTQLQDSENE	455
Db	626	NFSSGNEVYIDRIEFVPEV	645	Db	456	456 LPPEATGQPNEYSESYSHRLSHIGLISASHVKALV-- YSWTHRSADRTNTIBPNSITQIPLV	513
<hr/>							
RESULT 25							
ID	085796	PRELIMINARY;	PRT;	719 AA.	Qy	519 KAYALSGGASLIEGPGTGTGNNLFLKKESSNSIAKEFVTLNSAIIQLQYRIRYASTTNL	578
AC	085796;				514 KAFNLSSGAIVVRGPGTGGDL-L-RCTNTGTFGDLRVNIN_KPFFAQRYRIRYASTTDL	571	
DT	01-NOV-1998	(TrEMBLref)	08,	Created)	579 RLFVQ----NSNNDFLVYIINKTMKDDDLTVQFDLATTNSMGFSQDKNEELIGAE	632	
DT	01-MAR-2004	(TrEMBLref)	08,	Last sequence update)	572 QFHTSINGKAINQGN-----FSATMNRGEQEDLYDKTFRTVGFITPFSELDVQSTFTIGAW	625	
DE					633 SFVSNEKLYIDKIEFIPVQL	652	
GN					626 NFSSGNEVYIDRIEFVPEV	645	
OS	Bacillus thuringiensis	(subsp. kurstaki).					
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.						
OX	NCBI_TaxID:29333;						
RN							
SEQUENCE FROM N.A.							
RC	STRAIN=S101;				C1BA_BACTK	STANDARD;	PRT;
RA	Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;				ID C1BA_BACTK		1228 AA.
RL	Submitted (JUL-1-1998) to the EMBL/GenBank/DBJ databases.				AC P05577; Q45731;		
DR	BMBL; AF076953; AAC2910.1; -.				DT 01-FEB-1998 (Rel. 33, Last sequence update)		
DR	HSSP; P02965; 1C1Y.				DT 05-JUL-2004 (Rel. 44, Last annotation update)		
DR	GO; GO:0005102; F: receptor binding; IEA.				DE Pesticidal crystal protein cry1Ba (Insecticidal delta-endotoxin Go; GO:0006952; P: defense response; IEA.		
DR	GO; GO:0009405; P: pathogenesis; IEA.				DB Cry1Ba) (Crystalline entomocidal protein) (140 kDa crystal protein). Name-cry1Ba; Synonyms=cryA4, cryIBa;		
DR	InterPro; IPR001178; Endotoxin.				OS Bacillus thuringiensis (subsp. kurstaki), and		
DR	InterPro; IPR005638; endotoxin.				OS Bacillus thuringiensis (subsp. entomocidus).		
DR	InterPro; IPR005639; endotoxin_N.				OBacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
DR	InterPro; IPR008979; Gal bind_Like.				OC NCBI_TaxID=29339, 1436;		
PFam	PF03944; Endotoxin_C; 1.				RN [1] _Gal bind_Like.		
DR	PFam; PF03945; Endotoxin_N; 1.				RP SEQUENCE FROM N.A.		
DR	PFam; PF03945; Endotoxin_N; 1.				RC SPECIES=B.t.kurstaki; STRAIN=HD-2;		
KW	Plasmid.				RX MEDLINE=80203216; PubMed=3367680;		
SEQUENCE	719 AA;	81230 MW;	42746D478359BBA7	CRC64;	RA Bizard B.L., Whiteley H.R.,		
Query Matchscore 32.1%; Score 1094.5; DB 2; Length 719;							
Best Local Similarity 36.5%;	Pred. No. 5e-63;	Matches 248; Conservative 137;	Mismatches 232;	Indels 63;	RT Bacillus thuringiensis subsp. thuringiensis.		
Matches 248;	Length 719;			Gaps 19;	RN [2]		
SEQUENCE FROM N.A.							
Qy	1 MNPNNRSEHTDI-----KTPNSELOTNHNOYPLADNPNSTLEELNKFLRMTEDSS	53			RP SEQUENCE FROM N.A.		
Db	1 MLLKNODKQFQSNSNAKWDKISDSD-----LKNETDIELQNIHEDCLKMSBEYN	50			RC Soeterart P.;		
Qy	54 TE-VLDNSTVDAVGTVGIGVQYFLGKILGTVPPFAGALTTSFYQSFNLTWPSDADPWFMA	112			RA RT		
Db	51 VEPFVASTIQ---TGIGTAGKILGTVPPFAGQVSLYSPLGEWPKGKQWLFME	106			RL PROMOTER: Promotes colloidosmotic lysis by binding		
Qy	113 QVEVLIDKKEEYAKSKAKAELQGLQNNFEDYNAWNKWKPLSLRSKRSQDRIRELFS	172			CC epithelial cells of insects.		
Db	107 HYBEINODQISTYARNKALDQGLDAAVYHDLSLWSVG--NRNNTRAKSRSVQSYI	163			CC DEVELPMENTAL STAGE: The crystal protein is produced during		
Qy	173 QAESHPNMSPPAVSKPKEVLFPLPYAQANTHILLKDAQVFGEEGYSSSEDVAFYHR	232			CC sporulation and is accumulated both as an inclusion and as part of		
Db	164 ALELMFVQKLPSPPAVSGBEVPLPPIYAQANHLUURDASLFGKEWGLSSSEISFYNR	223			CC the spore coat.		
Qy	233 QLKLTQOQTDHCVNWYNGLNGLRGSYTDAYWKFNRERREMPLTVLDLIVLPPFYDIRY	292			CC MISCELLANEOUS: Toxic segment of the protein is located in the N-		
Db	224 OVERAGDYSDHCKWYSTGTLNLRGTRAEWSWTRYQFRDMTLMVLDLVALFPSYDQMY	283			CC terminus.		
Qy	293 SKGVKTTELTRDIFTD-----PIFSLNT-LQBYGPTFLSIENS-IRKPHLFDFLOGIE	342			CC SIMILARITY: Belongs to the delta endotoxin family.		
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EMBL; X06711; CRA29898.1; -.							

DR	EMBL; X95704; CAA65003.1; -.	DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DR	S00873; S00873.	DB	Cry1Ba.
DR	HSSP; P07130; 1DLC.	GN	Name=Cry1Ba.
DR	InterPro; IPR001118; Endotoxin.	OS	Bacillus thuringiensis.
DR	InterPro; IPR005638; endotoxin_C.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DR	InterPro; IPR005639; endotoxin_N.	OX	NCBI_TaxID=1428;
DR	InterPro; IPR008939; Gal_bind_Like.	RN	[1]
DR	Pfam; PF03944; Endotoxin_C; 1.	RP	SEQUENCE FROM N.A.
DR	Pfam; PF00555; Endotoxin_M; 1.	RA	Zhang J., Song F., Huang D.;
DR	Pfam; PF03945; Endotoxin_N; 1.	RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
KW	Sporulation; Toxin.	DR	Ar368257; AAK6351.1; -.
PT	VARIANT 150 Y -> H (In strain HD-110).	DR	HSPP; P07130; 1DLC.
SQ	SEQUENCE 1228 AA; 139647 MW; C8E3A19FB3D98575 CRC64;	DR	GO; GO:0005402; F:receptor binding; IEA.
	Query Match Score 1072.5; DB 1; Length 1228;	DR	GO; GO:000945; P:defense response; IEA.
	Best Local Similarity 36.6%; Pred. No. 2 9e-61;	DR	GO; GO:000555; P:Pathogenesis; IEA.
	Matches 246; Conservative 120; Mismatches 247; Indels 59; Gaps 19;	DR	Pfam; PF03944; Endotoxin_C; 1.
Qy	1 MNPNRNRSEHDTIKTPNSLQTQNINQYPLADNPNSTLEFLNKFELRMTEDSSTEVLNQ 60	DR	Pfam; PF00555; Endotoxin_M; 1.
Db	1 MTSAKRKNEIINAVSNHSAQMD-----LLPARDIESLCLAEAGNN---IDPF 45	DR	SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;
Qy	611 TVKDAVGTGTSVQGILGVGVPPFAGALTSPYQSPLNTIWPSPDKWAFMAQVEVLIDK 120	DR	Score 31.5%; Score 1071.5; DB 2; Length 1228;
Db	46 VSASTVQGTGINIAGRILGVGVPPFAGOLASFSYSLVGEWPRGRDOWTFLERVEOLINQ 105	DR	Best Local Similarity 36.6%; Pred. No. 3.e-61;
Qy	121 KIEEYAKSKALAEIQLGLQNLQNFEDTVNALNSWKTKPLSLRSKRSQDRIRE-LFSQL--AES 176	DR	Mismatches 246; Conservative 119; Mismatches 248; Indels 59; Gaps 19;
Db	106 QITENARNATLARIQLGLSFRAYQQSLEDWLE----NRDDARTSISVLYTOIALEL 158	DR	Matches 246; Best Local Similarity 36.6%;
Qy	177 HFRNSMSPSPAVSKPEVLFLPYTYAQAAANTHLIKDAQVEEENGSSSDVAEFPYHROLKL 236	DR	MTSNRKNEIINAVSNHSAQMD-----LLPARDIESLCLAEAGNN---IDPF 45
Db	159 4FLNAMPALPAIRNQVPLMVMVYAAQANLHLRDLASLGSGSERLTSQYEROVER 218	DR	61 TVKDAVGTGTSVQGILGVGVPPFAGALTSPYQSPLNTIWPSPDKWAFMAQVEVLIDK 120
Qy	237 TQQYTDHCYCNWNYNGLNGRGSTYDWTWYKFRERMTLTVDLIVLPFYD1RLYSKGV 296	Db	46 VSASTVQGTGINIAGRILGVGVPPFAGOLASFSYSLVGEWPRGRDOWTFLERVEOLINQ 105
Db	219 TRDSDYCBEWNNTGLNSLRGTTNAASWRYNQFRDLTLGVLDLVLPFYDTRTYPINT 278	Qy	121 KIEEYAKSKALAEIQLGLQNLQNFEDTVNALNSWKTKPLSLRSKRSQDRIRE-LFSQL--AES 176
Qy	297 KTELTRDIFTDP1-----FSLNLTQEYQGPTFLSIE-NISRKRPHLFDLQGIEBFHTRLQ 348	Db	106 QITENARNATLARIQLGLSFRAYQQSLEDWLE----NRDDARTSISVLYTOIALEL 158
Db	279 SAQLTREVYDTAIGATGVNMASHWNWNMAPSFAIEAAIRSPHLLDFLEQLTIFS_AS 337	Qy	61 TVKDAVGTGTSVQGILGVGVPPFAGALTSPYQSPLNTIWPSPDKWAFMAQVEVLIDK 120
Qy	349 PGYFKGDSSPFWNSGNYVETRSPSIGSSKT1SPFYG--DKSTTEPVQKLSFGOKVYRTIAN 406	Db	46 TQQYTDHCYCNWNYNGLNGRGSTYDWTWYKFRERMTLTVDLIVLPFYD1RLYSKGV 296
Db	338 SRWANTRHTWYWRHTIQRSPIGGLNST--HGATATINSVP-TURFASDQYRTESY 393	Qy	237 KTELTRDIFTDP1-----FSLNLTQEYQGPTFLSIE-NISRKRPHLFDLQGIEBFHTRLQ 348
Qy	407 TDVAAWPNCKVYL---GVTKVDFESQYDDQK-NETSTQTYDTSKRNNGHVSAQDSIDQLP 461	Db	219 TRDSDYCBEWNNTGLNSLRGTTNAASWRYNQFRDLTLGVLDLVLPFYDTRTYPINT 278
Db	394 AGVLLW---GIVYLEPIHGPYTFRENETNEQNSIDRGTAHYSQYESPGLQDSETELPP 450	Qy	297 KTELTRDIFTDP1-----FSLNLTQEYQGPTFLSIE-NISRKRPHLFDLQGIEBFHTRLQ 348
Qy	462 ETIDBPLEXKAYSHQUNYAECFLMODRGT1PFPTWTHSSVDFNTIDAKITOLPVVKAY 521	Db	279 SAQLTREVYDTAIGATGVNMASHWNWNMAPSFAIEAAIRSPHLLDFLEQLTIFS_AS 337
Db	451 ETTERPNYTSYSHRLSHQUNIYLQS--RVNVPUVSWTHRSADRNTTIGPRITQIPMYKAS 508	Qy	177 HFRNSMSPSPAVSKPEVLFLPYTYAQAAANTHLIKDAQVEEENGSSSDVAEFPYHROLKL 236
Qy	522 ALSSGASITLEGGFTGGNLLFLKESSNSIAKFKVTLNSAALLQYRYRIRYASTTNLRLF 581	Db	159 4FLNAMPALPAIRNQVPLMVMVYAAQANLHLRDLASLGSGSERLTSQYEROVER 218
Db	509 ELPGQTTVVRGPFTGGDIL-RRNTGCFGP1RVTW-GPLTQYRIGFRASTVDFDFF 566	Qy	219 TRDSDYCBEWNNTGLNSLRGTTNAASWRYNQFRDLTLGVLDLVLPFYDTRTYPINT 278
Qy	582 VQNSN--NDELVIYINKTMNKKODDLITYQFDLATTNSMGSGDKNELLIGAESFVSNE 638	Db	407 TDVAAWPNCKVYL---GVTKVDFESQYDDQK-NETSTQTYDTSKRNNGHVSAQDSIDQLP 461
Db	567 VSRGGTTVNNFRFL--RMNNSGDELKYCNEVRRAFTPFTFQIODIIRTSTQGLSGNG 623	Qy	462 ETIDBPLEXKAYSHQUNYAECFLMODRGT1PFPTWTHSSVDFNTIDAKITOLPVVKAY 521
Qy	639 KIYDKEIEIPV 650	Db	394 AGVLLW---GIVYLEPIHGPYTFRENETNEQNSIDRGTAHYSQYESPGLQDSETELPP 450
Db	624 EVYDKEIEIPV 635	Qy	522 ALSSGASITLEGGFTGGNLLFLKESSNSIAKFKVTLNSAALLQYRYRIRYASTTNLRLF 581
	PRELIMINARY;	Db	509 ELPGQTTVVRGPFTGGDIL-RRNTGCFGP1RVTW-GPLTQYRIGFRASTVDFDFF 566
RESULT 27	Q9NNM5	Qy	567 VSRGGTTVNNFRFL--RMNNSGDELKYCNEVRRAFTPFTFQIODIIRTSTQGLSGNG 623
AC Q9NNM5;	PRELIMINARY;	Db	639 KIYDKEIEIPV 650
DT 01-DEC-2001 (TrEMBLrel. 19, Created)	PRT;	Qy	Q9NNM5
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	1228 AA.		AC Q9NNM5;

DR	Pfam; PF03944; Endotoxin_C; 1.	RL Submitted (JAN-2004) to the EMBL/GenBank/DBDJ databases.
DR	Pfam; PF00555; Endotoxin_M; 1.	DR EMBL; AY518201; AA987833; 1;
DR	Pfam; PF03945; Endotoxin_N; 1.	DR GO; GO:0005102; F-receptor binding; IFA.
KW	Direct protein sequencing; Sporulation; Toxin.	DR GO; GO:0006932; P-defense response; IFA.
SQ	SEQUENCING 1160 AA; 130425 MW; C16CDB912EEB8751 CRC64;	DR InterPro; IPR009079; 4-helix cytoxine.
Query Match	31.1% Score 1060; DB 1; Length 1160;	DR InterPro; IPR011178; Endotoxin_T.
Best Local Similarity	37.1%; Pred. No. 1.8e-60;	DR InterPro; IPR005638; endotoxin_C.
Matches 254; Conservative 116; Mismatches 254; Indels 60; Gaps 21;	DR InterPro; IPR005639; endotoxin_N.	
Qy	1 MNPNRSEHDITIKTPNSSELTQTNHQYPADNPNSTLELNKYEFLRMLTIVPS-DADPKAFMAOYE 115	DR InterPro; IPR008919; Gal_bind_Like.
Db	61 GTFPSAQDAVGTTGDIVSTTISGQIPVPGFVTSLSGLIUMPSNNENWQFMNRE 120	DR Pfam; PP03944; Endotoxin_C; 1.
Qy	116 VLIDKKIEYAKSALKAAELQGLQNNFEDVNALNSWKCPPLSLRSKRSQRDRIELFSQAE 175	DR Pfam; PP00555; Endotoxin_M; 1.
Db	121 ELIDKILDSVRSRAIDLANSRAVEYYQNALEDDWRKPP--HSTRSALVAKERGNAE 177	DR Pfam; PP03945; Endotoxin_N; 1.
Qy	61 ---TVKDAGVTGTSVYCGOILGVGVPPFAGALTFSYQSFNTIIPS-DADPKAFMAOYE 115	SEQUENCE 1160 AA; 130452 MW; C794F99AD1397188 CRC64;
Db	61 MNPNNQNEYIIIDALSPSVSDNSTRYPLANDQNTNLQMMNYKDYLKRTESTNAELSRRP 60	Query Match 31.1%; Score 1060; DB 2; Length 1160;
Qy	61 MNPNRSEHDITIKTPNSSELTQTNHQYPADNPNSTLEPLNYYEFLRMLTIVPS-DADPKAFMAOYE 115	Best Local Similarity 37.1%; Pred. No. 1.8e-60;
Db	61 GTFPSAQDAVGTTGDIVSTTISGQIPVPGFVTSLSGLIUMPSNNENWQFMNRE 120	Matches 254; Mismatches 254; Indels 60; Gaps 21;
Qy	61 MNPNNQNEYIIIDALSPSVSDNSTRYPLANDQNTNLQMMNYKDYLKRTESTNAELSRRP 60	Qy 1 MNPNRSEHDITIKTPNSSELTQTNHQYPADNPNSTLEPLNYYEFLRMLTIVPS-DADPKAFMAOYE 115
Db	61 GTFPSAQDAVGTTGDIVSTTISGQIPVPGFVTSLSGLIUMPSNNENWQFMNRE 120	Db 1 MNPNNQNEYIIIDALSPSVSDNSTRYPLANDQNTNLQMMNYKDYLKRTESTNAELSRRP 60
Qy	116 VLDKIKIEYAKSALKAAELQGLQNNFEDVNALNSWKCPPLSLRSKRSQRDRIELFSQAE 175	Qy 116 VLDKIKIEYAKSALKAAELQGLQNNFEDVNALNSWKCPPLSLRSKRSQRDRIELFSQAE 175
Db	121 ELIDKILDSVRSRAIDLANSRAVEYYQNALEDDWRKPP--HSTRSALVAKERGNAE 177	Db 121 ELIDKILDSVRSRAIDLANSRAVEYYQNALEDDWRKPP--HSTRSALVAKERGNAE 177
Qy	61 ---SHFRNSMSPSPAVSKPSKEVLLPEPTYAQANTHLLKDAQVFGEEGYSSSEDAEYHRQLK 235	Qy 176 SHFRNSMSPSPAVSKPSKEVLLPEPTYAQANTHLLKDAQVFGEEGYSSSEDAEYHRQLK 235
Db	178 AILRTNMGGFSQTQNYETPTLPPTYAQAASLHLVNRDVQTYKGKWPONDIDLFYKEQVS 237	Db 178 AILRTNMGGFSQTQNYETPTLPPTYAQAASLHLVNRDVQTYKGKWPONDIDLFYKEQVS 237
Qy	236 LTQQYTDHCVNWNVNGLNGLRGSTYDAWTKFNRFRMELTIVLDLVLFPPDYIRLYSKG 295	Db 236 LTOOYTDHCVNWNVNGLNGLRGSTYDAWTKFNRFRMELTIVLDLVLFPPDYIRLYSKG 295
Db	238 YTARYSDHCVQWTNAGLNKLRTGAKQWVYNRPREMVNVMDLVALEPNTYARIPEL 297	Db 238 YTARYSDHCVQWTNAGLNKLRTGAKQWVYNRPREMVNVMDLVALEPNTYARIPEL 297
Qy	296 VKTTELTRDIFTDPFISLNTLQE-----YG-----PTFLSIENSIRKPHLFDYLOGIEF 343	Qy 296 VKTTELTRDIFTDPGSSYVYQGSSTLISWDMIPAALPSSTLNLLRKFDTFTLLOEIR 357
Db	298 TNAABTETRDLRDPGSSYVYQGSSTLISWDMIPAALPSSTLNLLRKFDTFTLLOEIR 357	Db 298 TNAELTRDIFTDPGSSYVYQGSSTLISWDMIPAALPSSTLNLLRKFDTFTLLOEIR 357
Qy	344 HTPL-QPGYFGKDSFNTWGSQYVETRPSIGKSS-KTITSPFYQKLSFDGQK-V 400	Qy 344 HTPL-QPGYFGKDSFNTWGSQYVETRPSIGKSS-KTITSPFYQKLSFDGQK-V 400
Db	358 YTSFRQNGTI--EXYNMNGQRLTTSIYGGSFNKSYGLAGADEIIV-----GNDI 409	Db 358 YTSFRQNGTI--EXYNMNGQRLTTSIYGGSFNKSYGLAGADEIIV-----GNDI 409
Qy	401 YRTANTDVAAPNGKVYUVTKVDFSQYDQNETSTQTYDS-KRNGHVSAAQSDIDQ 459	Qy 401 YRTANTDVAAPNGKVYUVTKVDFSQYDQNETSTQTYDS-KRNGHVSAAQSDIDQ 459
Db	410 YRVWW-TYIGRTYS-LIGVNPNPF--YSNNNTQKTYTSKPKQFAGIKTIDSGBEL 461	Db 410 YRVWW-TYIGRTYS-LIGVNPNPF--YSNNNTQKTYTSKPKQFAGIKTIDSGBEL 461
Qy	460 PPETTDEPLEKAYSHOLNAYAECFLMQDRGT----IPFTTWTHRSVDFFNTIDAEKITOL 515	Qy 460 PPETTDEPLEKAYSHOLNAYAECFLMQDRGT----IPFTTWTHRSVDFFNTIDAEKITOL 515
Db	462 TYEN----YQSTSHRVSTSITSFEIKLSTGTVGUVPIGWTHSASSINNFYATKLSQI 516	Db 462 TYEN----YQSTSHRVSTSITSFEIKLSTGTVGUVPIGWTHSASSINNFYATKLSQI 516
Qy	516 PVVKAYALSSGA--SIEPGPGFTCGNLLFKESSNSIAKEKFTULNSAALLQRYVRIRYA 573	Qy 516 PVVKAYALSSGA--SIEPGPGFTCGNLLFKESSNSIAKEKFTULNSAALLQRYVRIRYA 573
Db	517 PINKASRTSGAVWNFOEGL-YNGGPVNKLSGSGSQVINLRYVATDAKGASQVRIRYA 575	Db 517 PINKASRTSGAVWNFOEGL-YNGGPVNKLSGSGSQVINLRYVATDAKGASQVRIRYA 575
Qy	574 S-----TINLRLFQVNSNDFLVIYINRNMKDDLTYQTPDLATMS-NMGFGSDRN 626	Qy 574 S-----TINLRLFQVNSNDFLVIYINRNMKDDLTYQTPDLATMS-NMGFGSDRN 626
Db	576 SDRAKGFTSSRSPENPATSYASTAYTN-TMSTNASLTYSTPAYAESGPINLGSSSRT 634	Db 576 SDRAKGFTSSRSPENPATSYASTAYTN-TMSTNASLTYSTPAYAESGPINLGSSSRT 634
Qy	627 LIIGAEPSVNEKYYIDKIEFIPV 650	Qy 627 LIIGAEPSVNEKYYIDKIEFIPV 650
Db	635 FDISITKEAANLYIDREFIPV 658	Db 635 FDISITKEAANLYIDREFIPV 658
RESULT 30		
ID	O6R2R6	PRELIMINARY; PRT; 1160 AA.
AC	Q6R2R6	
Q6R2R6;		
05-JUL-2004	(TREMBrel. 27, Created)	
05-JUL-2004	(TREMBrel. 27, Last sequence update)	
05-JUL-2004	(TREMBrel. 27, Last annotation update)	
DE	Bacillus thuringiensis	
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
NCBI_TaxID	1428;	
OX		
[1]		
DT		
SEQUENCE FROM N.A.		
RP		
RA		
Song F., Shu C., Zhang J.;		
RESULT 31		
QBKNY2		
ID	QBKNY2	PRELIMINARY;
AC	QBKNY2;	PRT; 1231 AA.
DT	01-OCT-2002 (TREMBrel. 22, Created)	

Qy	637 NEKTYIDKIEFIPV 650	Db	629 NAEVVIDRFFEFIPV 642
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DB	CRYBII;	GN	Bacillus thuringiensis,
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	OC	NCBI_TaxID:1428;
OX	[1] _	RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RA	Isakova I. A., Isakov Y.B., Rymar' S. E., Yarovoi S. V.;
RL	Submitted (AUG-2002) to the EMBL/GenBank/DDJB databases.	DR	HSSP; AY18457; AAM93496.1; -.
RL	HSPP; P02865; ICIY.	DR	GO; GO:0005102; F: receptor binding; IEA.
DR	GO; GO:0009450; P: defense response; IEA.	DR	GO; GO:0009405; P: pathogenesis; IEA.
DR	InterPro; IPR001178; Endotoxin.	DR	InterPro; IPR005638; endotoxin.
DR	InterPro; IPR005639; endotoxin_N.	DR	InterPro; IPR008979; Gal_bind_Like.
DR	Pfam; PF00944; Endotoxin_C; 1.	DR	Pfam; PF00555; Endotoxin_M; 1.
DR	Pfam; PF03945; Endotoxin_N; 1.	DR	SEQUENCE 1231 AA; 139764 MW; C9F284BA9297EA00 CRC64;
SQ	SEQUENCE 1231 AA; 139764 MW; C9F284BA9297EA00 CRC64;	Qy	1 MNPNNSSEHDITKVTPNSELTQTHNQPLADNPNSTLLELNKYKEFLMTEDS---STEV 56
Qy	1 MTSNRKNEELI----NALSIEPTVSNPST---QMNLSPDARI-EDSLCVAEVNN 46	Db	57 LDNSTVKDAVGIGISVQGILGVGVPPAGALTFSYQSFNLNTWPSDADPKAFMAQEV 116
Qy	47 IIPPFVSASTVQCGINIAIGLIGVGVPAQASFSYLVEWPSGRDPWEFLHEVQ 106	Db	117 LIDKKIREYAKSKAAELQGLONNWSKCTPLSLRSKSDRIRFLFSQAS 176
Qy	117 LIDKKIREYAKSKAAELQGLONNWSKCTPLSLRSKSDRIRFLFSQAS 176	Db	107 LIRQQVENTRNTRTAIRLEGGRGYRSYQQALETWLD--NRNDARSRSTILERYVAEL 163
Qy	177 HFRNSMPDFAVSKFEVLFLPVTQAAQANTHLLIJKDQAQVGEENGYSSEDVAEYHROLKL 236	Dr	177 HFRNSMPDFAVSKFEVLFLPVTQAAQANTHLLIJKDQAQVGEENGYSSEDVAEYHROLKL 236
Db	164 DTTAIPFLPRINEEPVLMVYQAAANTHLIILRDAISFGSEGMASSDNQVYQEBQIRY 223	Dr	164 DTTAIPFLPRINEEPVLMVYQAAANTHLIILRDAISFGSEGMASSDNQVYQEBQIRY 223
Qy	237 TOOYDHCVNTWNVNGLQRGSTYDAWKENRFREMTLVTLIDLIVLPFYDYLRLYSKV 296	Db	237 TOOYDHCVNTWNVNGLQRGSTYDAWKENRFREMTLVTLIDLIVLPFYDYLRLYSKV 296
Qy	224 TPEYSNMHQVWNTGUNLRGTAESWRYQPRRDITLVGLVPSYSDTRTPINT 283	Db	224 TPEYSNMHQVWNTGUNLRGTAESWRYQPRRDITLVGLVPSYSDTRTPINT 283
Qy	297 KTELTRDIFTDPI-----FSLNTLQEQYGPFLSTNSI-RKPHLFYLOGIEFHTR 346	Db	297 KTELTRDIFTDPI-----FSLNTLQEQYGPFLSTNSI-RKPHLFYLOGIEFHTR 346
Qy	284 SAQLTREYTDPIGRTNAPSGFASNWNNNAASFSAEAIFPRPHLDPPEQLTIY- 342	Db	284 SAQLTREYTDPIGRTNAPSGFASNWNNNAASFSAEAIFPRPHLDPPEQLTIY- 342
Qy	347 LQPGYFGKDSENVWSQHNVETRPSIGSSKTITSPEYQKLSFDGOKVYRTIAN 406	Db	347 LQPGYFGKDSENVWSQHNVETRPSIGSSKTITSPEYQKLSFDGOKVYRTIAN 406
Qy	343 ASSRWSSTQHMMWGHRLNFRIGGTNTSTOGTNTNTSINPV-TLQFTSDRVYRTSN 401	Db	343 ASSRWSSTQHMMWGHRLNFRIGGTNTSTOGTNTNTSINPV-TLQFTSDRVYRTSN 401
Qy	402 A-----GTVLLETFPTPQVDPDRENTPQNTYERGATYPSQYQGIGQIQFDSETBL 459	Db	402 A-----GTVLLETFPTPQVDPDRENTPQNTYERGATYPSQYQGIGQIQFDSETBL 459
Qy	460 PPETTDEPLEKAYSHQMLNYAECFLMMDQDRGTTIPPTWTHRSVDFPNTDAEKITQLPVVK 519	Db	460 PPETTDEPLEKAYSHQMLNYAECFLMMDQDRGTTIPPTWTHRSVDFPNTDAEKITQLPVVK 519
Qy	455 PPITERNNYESYSHRLSHIGLIGNTRA--PVYSSWTHSADRNTNIGPNRITQIPAVK 512	Db	455 PPITERNNYESYSHRLSHIGLIGNTRA--PVYSSWTHSADRNTNIGPNRITQIPAVK 512
Qy	520 AVALSSGASITIEPGFTGKVNLLFKESSNSIAK---FKVTLNSALLORYVRIRYASIT 576	Db	520 AVALSSGASITIEPGFTGKVNLLFKESSNSIAK---FKVTLNSALLORYVRIRYASIT 576
Qy	513 GRLFLNG-SV1SGPFGTCDGVRLNRNNGNQNRGYIEP1QFTSTSTRYVRVRYASIT 571	Db	513 GRLFLNG-SV1SGPFGTCDGVRLNRNNGNQNRGYIEP1QFTSTSTRYVRVRYASIT 571
Qy	577 NLRLFQNSNDLFLVIVYINKTMKDDDLTYQTFDLATINSMGMSGDKNELLIGAESFYS 636	Db	577 NLRLFQNSNDLFLVIVYINKTMKDDDLTYQTFDLATINSMGMSGDKNELLIGAESFYS 636
Qy	572 SIEFLNVQGNSNDFIPTNTLUPATAASLSDN--QSGFEGYVBNNAATISATGN-IVGARNFSA 628	Db	572 SIEFLNVQGNSNDFIPTNTLUPATAASLSDN--QSGFEGYVBNNAATISATGN-IVGARNFSA 628
Qy	54 TEVLIDKIEYAKSKAAELQGLONNFEDVNAWSKKTPLSLSKRSQDRIRELFSQ 173	Db	54 TEVLIDKIEYAKSKAAELQGLONNFEDVNAWSKKTPLSLSKRSQDRIRELFSQ 173
Qy	51 ---IDFVSASTIQGIGIAGKILGTGVPPFGQIISLYSFLIGKLGWMPKGKSQWEITMEH 107	Db	51 ---IDFVSASTIQGIGIAGKILGTGVPPFGQIISLYSFLIGKLGWMPKGKSQWEITMEH 107
Qy	114 AEHPNSMPSFAVSKFEVLFLPVTQAAANTHLLIJKDQAQVGEENGYSSEDVAEYHRO 224	Db	114 AEHPNSMPSFAVSKFEVLFLPVTQAAANTHLLIJKDQAQVGEENGYSSEDVAEYHRO 224
Qy	108 VEA1NPKISTYARNKALTDLKGLGIALAVYTHELESWSVG--NRNTRARSVYXIA 164	Db	108 VEA1NPKISTYARNKALTDLKGLGIALAVYTHELESWSVG--NRNTRARSVYXIA 164

Qy	234 LKLTOOYTIDCHVNWVNVGLRGLRGSTYDWAUKENFRERMTLTVDLIVLFPPFDIYLX 293	DR HSSP; P02965; 1CY.
Db	225 VERTDYSVCVKVNNTGLNRLRATNGQSWVRYNQFRKIEMLVMDLVRFPSYDLYV 284	DR InterPro; IPR011778; Endotoxin.
Qy	294 KGVTBTLTDIRDPIFSNLTLQ-----EVGPTFDSLQGIEF 343	DR InterPro; IPR005638; endotoxin_C.
Db	285 IKTSOLTEREVTDAGITDVPNQLRSTWYNNNAPSFAIEAVIRSHLLEFLKTY 344	DR InterPro; IPR008979; Gal bind like.
Qy	344 HTRIOPGYFGKDSFNYWSGNVYETRPSIGSSKTISPFYGDKST--EPYOKLUSFDGOKVY 401	DR Pfam; PF03944; Endotoxin_C; 1.
Db	345 YSLIS-RWMSNTQYAMMGGHRLSPIGGALNTSQ---GSTNTSINPA-TLQFTSRDYE 399	DR Pfam; PF00555; Endotoxin_M; 1.
Qy	402 RTIANTDVAAPWNKGKVYL----CVTKVDFQSQYDQKNETSTQTYDSTSKRKNNGHVSA --- 452	DR Pfam; PF03945; Endotoxin_N; 1.
Db	400 RT-----BSWAGUNLFLTOPVNGVPRVD---HWFKEPLTLPIASDNFVYLGAGVGTOL 449	KW Sporulon>Toxin.
Qy	453 QPSIDQLPDETTDEPLEKAYSHQLYNAYECPFLMDQRGTTLPFTWTHRSVDFFTNDAEKI 512	SEQUENCE 1231 AA; 139654 MW; 129A0371CDDBBB52 CRC64;
Db	450 QDSNEELPBPETTGQPNYESYSHRLSHIG--LISGSVHVKALLYSVTHRSRADRTNTIEPNSI 507	Query Match 30.6%; Score 1042; DB 1; Length 1231;
Qy	513 TQLPVVKAVALSSGASIIISPGFTGNNLJFLKESSNSIAKFKVTLNSAALLQYRVIRY 572	Best Local Similarity 35.5%; Prod. No. 2.9e-59;
Db	508 TQIPVKATNLSSGAVVPGFPFTGHHI-.RRTYSGTFHIRNIN-PPFAQRXVRNMISY 565	Matches 239; Conservative 120; Mismatches 260; Indels 54; Gaps 16;
Qy	573 ASTTNLRFLRQV----NSNNDFLIVYINKTMNKODDLTYOTFPLATNNNSNGFSGDKE 626	Query 1 MNPNRNRSEHDHTKVTNPSELQTHNQYPLADNPNSTL--EINYKETLRTMDSSTEVL 57
Db	566 ASTTDLQFHTSINGRAINSQDN----FSATMNREGDLYDKTFRGTTTGFPSFSDVQT 619	Db 1 MTSNRKNEII-----NALSIAPVNSHSAOMLSLDARIEDSUCIAEGNNINPL 50
Qy	627 LIIGAESFSNEKYYIDKBFPIYOL 652	Qy 58 DNSTVKDADVGTG-SVVGQILLGUVGVPPAGALTFSYQSFNTIWPSADDWKAFMAQAEVL 117
Db	620 FTIGAWNFSGGNEVYIGREFVPPVVEV 645	Db 51 VSAS---TVQTGGINAIGRLGVILGVPPQGLASFYFLVGLMPGSDPWEILLEVEQL 107
Qy	RESULT 33	Qy 118 IDKKIEEYAKSKALAELQGLQNNFEDYNNALNSWKTPTLSRSKRSQDRIRELFSQAASH 177
C1BD_BACTZ	ID C1BD_BACTZ STANDARD; PRY; 1231 AA.	Db 108 IROQQTENTRNTAIARLEGRLGRGRYRSCQALETWL D--NRNDARSSTILERYVALELD 164
AC	O92A25;	Qy 178 PRNSMPSPAVSKPEVFLPFTYQAOANTHILLKDAQVGEENGYSSEDVAEYFHQLKT 237
DT	30-MAY-2000 (Rel. 39, Created)	Db 165 ITTAIPFLPRIRNEBVPLMMVYQAANLHLRLDASLFLGSEMASDVNOYYQEQLRYT 224
DT	30-MAY-2000 (Rel. 39, Last sequence update)	Qy 238 QQYTDHCYCNWVNWGLNGLRGSTYDAWYKFNRFREMLTVLDFLIVLFFDYLRLYSKAVK 297
DT	05-JUL-2004 (Rel. 44, Last annotation update)	Db 225 EBYSNHCQVWNTGLANNLRGTAESLWYNQFRDLTILGVLDIVLFFSYDIRTYPINTS 284
DE	Pesticidal crystal protein cry1Bd (Insecticidal delta-endotoxin Cry1B(d)) (Cry1B(d); Synonyms=cryEl, cryTB(d), cRYLA1; Name=cry1Bd; Subsp. wuhanensis) (Subsp. wuhanensis).	Qy 298 TELTRDIFTDP-----FSLNLTQEQYGPFLSIENSI-RKPHLFDPYLOGIEFHTRL 347
GN	Bacillus thuringiensis (Subsp. Baciillaceae; Bacillus.	Db 285 AQJRTREITDPIGRTNAPSGFASTNWNNNAPSFALEAAIFRPHLDFPBQJTIYS-A 343
OC	NCBI_TAXID=52024;	Qy 348 QPGYFGKDSFNTWMSGNVYETRPSIGSKKTISPFYGDKSTEPVQKLSFGQKVRTIANT 407
RN	[1]	Db 344 SSWWSTSTQHMNTWVGHLNFRPIGGTNTSTQGLNTNTSINPV-TLQFTSDYRTYTESNA 402
RP	SEQUENCE FROM N.A.	Qy 408 DVRAWPNKVKYLGVTYD-----FSQYDDQK-NESTQTYDTSKRNNGHVSADDSIDOLP 460
RC	STRAIN=ID-525;	Db 403 -----GTNLIFTPTPVGVPWRFNTPQNPVYERGATTYSQPYGVGQIQLFDSETELP 455
RX	MEDLINE=20153386;	Qy 461 PETTDEPLEKAYSHQLYNAYECFLMODRGTIPFFTWTHRSVDFFTNDAEKITQLPVYKA 520
RA	KUO W.-., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.; "Cloning of two new cry genes from Bacillus thuringiensis subsp. "wuhanensis strain.", Curr. Microbiol. 40:227-232(2000).	Db 456 PETTERPYNEYSFHRLSHIGLIGNTEA--PVWSWTHRSADRTNTIGPNRITQIPAVKG 513
RT	-I- FUNCTION: Promotes colloidomotic lysis by binding to the midgut epithelial cells of lepidopteran larvae. Toxic to <i>Plutella xylostella</i> .	Qy 578 LRIFPVQNSNNDFLVIYINKTMNKDDLTQYTEDLATNTSMCMFGSDGNELIGAESFVSN 637
RT	-I- DEVELOPMENTAL STAGE: The crystal protein is produced during the spore coat.	Db 573 IEIINVGNSSNIFTNTLUPATAASLDNU--QSCDFGKVBEINNAFTSATGN-IVGARNFSAN 629
CC	-I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	Qy 638 EKIYIDKIEFIPV 650
CC	-I- SIMILARITY: Belongs to the delta endotoxin family.	Db 630 AEVTDIDRFEFIPV 642
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RESULT 34
CC	CC C9DA_BACTP	CC ID C9DA_BACTP STANDARD; PRT; 1169 AA.
CC	CC 00614;	CC DT 30-MAY-2000 (Rel. 39, Created)
CC	CC RFLFNG-SVISGSGFTGDDVWRLNRNQNQIQRGYEVPIQFTSTSTRVVRVYASVTS 572	CC DT 30-MAY-2004 (Rel. 44, Last sequence update)
CC	CC 578 LRIFPVQNSNNDFLVIYINKTMNKDDLTQYTEDLATNTSMCMFGSDGNELIGAESFVSN 637	CC DE Pesticidal crystal protein cry9Da (Insecticidal delta-endotoxin CryIXD(a)) (Crystalline entomocidal protein) (132 kDa crystal
DR	EMBL; U70726; AADD0292.1; - .	DE

Db	121	ELIDQRISSEQVRNALDAALGHDHYNEVLAALBEWLERPNGARANLAFQR----FENIH 176	Qy	1	MNPNNRSEHDTIKVTPNSELTQTNHQYPLADPNSTLE--ELNYKEFLRMTEDSLSTEVL 57
Qy	176	SHFNRNSMPF---AVSKKEVLFLPTYQAQANTHLLKDKAQVFGEEWGSSEDVAEYH 231	Db	1	MTSIRKNENEII-----NALSIPAVSNHSIAQMNUSTDARIEDSCTIAEGNN---I 47
Db	177	QLFYSQMPFGSGPCSERDAAVALLTVYQAQANLHLLLKDAEYARGARLNQOINLYFN 236	Qy	58	DNSTVKDAVGTTGIVSGQILGVNGVPEAGALTSPYQSFINTINTPSDADPKAFAQVEYL 117
Qy	232	RQLKLQQMTDHCYCNWYNGLNGLRGSTDIAWKVNREREMTILTVLDLIVLPFYDIRL 291	Db	48	DFFVSASTQTGGINAIGRLGVCPFAQIASFSFLVGEMLPRGRDEWEIFLHVEQL 107
Db	237	AQDRTQITNNHCVATYNRGNLENURGTNTESWYHQAERETILMADIVALPYNIRQ 296	Qy	118	IDKKEEYAKSKALABLCOLQNMFDYNAISWKTPLSLRSKRSDQIRE-LFSQ-- 173
Qy	292	YSKGKVKTTELTRDIFTDPFLSNTLQTYEG-----PTFLSTENS-TRKPHLFDLQG 340	Db	108	IRQQVTENTRTDALARGLGLNSFRAYQOSLEDWL-----NRDDARTRSVLYTQYIA 160
Db	297	YPNGANPQLQTRIYTDpVW-FNPNPANOGLCRRMWNPPMTFSELENTPRPHLFDRANS 355	Qy	174	AESHFIRNSMPSFAVKSFEPVLFPTYQAQANTHLLKDAQVFGBEWGYSSEDVAEFYHQ 233
Qy	341	IEFHTRLQCYGFDSFNWGNVYETRSIGSSKTISSPFYGDKSTEPVQKLSFDGKRY 400	Db	161	LELDFLNAMPLFAIRNQEYPLMVAQAQANLHLLRDLASFSESEFGLTQSDFRYYERQ 220
Db	356	LTMNSHHRF--ISSNFMWDAGH-----TURRSYNNNSA--VOEDSYGATT S 398	Qy	234	LKLTOQYTDHCVNMYNVGLNLRGSTYDAWKVKNREREMTILTVLDLIVLPFYDIRLYS 293
Qy	401	YRTTANTDAAPNGKVTIQLVTKYDFSQ-----NETSTOTYDSKRN 446	Db	221	VEKTREYSDCYARWNTGUNLNRTGNAESWLRVQFRDLTLGVLVALFSPSTDRYV P 280
Db	399	TRVTTINTGV---NGTNNTIESTAVDFRSCLLGYGVHRAFSVFGGLEPGNTI----SPAN 449	Qy	294	KGVKTELTRDIFTDPF-----FSLNTLQBYGPTLUSIENS-TRKPHLFQYLG3IEP 343
Qy	447	NGHVSQAQDIDOLQP-PETTDEPLEKEYASHQLYNAECFL--MODRRGTI-----PFTFTW 497	Db	281	MNTSAQUTREIYTDPIGRNTNAPSFASTNWNNNAPPSAIEAVIRPHLJDFPEQLUTI 340
Db	450	AGCRNLHDTRDPLEENNGSP-----SHRLSHV-TFLSLFTDQASGTRNSGAVPLYWA 503	Qy	344	HTRUQPGYFGKOSFNYWGSNYYVETRPSIGSKTITSPFYGDKST--EPVQKULSEDGQKVY 401
Qy	498	HRSVDEFNTIDAKITOLPFPVKAVALSSGASLIEGPGFPGNLLFLKESNSNASTAKFVTL 557	Db	341	FSVLS-RWSNTQYMNWYGHRLERSITRGLSLST-----HGNTNTSINPV-TLQFTSRDVY 395
Db	504	RQDIDLNNTITANRITQFLPKVASEIAACTTIVVRGPGETGGDL-RRTSAGTLGTTIRNV 562	Qy	402	RT-----IANTDVA-----WP-----GKTY-LGVTKVDFQSQYDDQKNETST 438
Qy	558	NSAIIQLQRVVRVRYASTNLRLFVQNSNDFLVYIYINKTMKDDDTYQFDLATNSN 617	Db	396	RTESSAGINILLLTPVNGVPWAREFNWNPLNSLRSLLXTTGTV-----GT 443
Db	563	NS-PLTQRVVRVRFYASTDFNFNQFLVQNSNDFLVYIYINKTMKDDDTYQFDLATNS 621	Qy	439	QYDSDKRNIGHYSAQDSDIDQLPBTETDPLEKAYSHQLYNAYCFLMDQRRG1IPPFWTW 498
Qy	618	MGFSGDKNHELIIGAESFSVSYNEKLYIDKIEFIPV 650	Db	444	QLPDS-----TELPETPETPNYESHRLSNIR-LISGNTLRAPVYWSHTH 489
Db	622	FNFQIQDTRLRLTVQSFSSQQVYVDRIELIPV 654	Qy	499	RSYDFNTIDAKITQLPVKAVALSSASASILEGPFTGQNLFLKESNSNIAKFKVTLN 558
Db	RESULT 36				
Q6TYW8		PRELIMINARY;	PRT;	849 AA.	
ID	Q6PYW8				C1BE_BACTU STANDARD; PRT; 1227 AA.
AC	Q6PYW8;				ID C1BE_BACTU 085805;
DT	05-JUL-2004	(TREMBrel. 27, Created)			DT 16-OCT-2001 (Rel. 40, Created)
DT	05-JUL-2004	(TREMBrel. 27, Last sequence update)			DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT	05-JUL-2004	(TREMBrel. 27, Last annotation update)			DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB	CryIB type crystal protein (Fragment).				DE Pesticidal crystal protein cryIBe (Insecticidal delta-endotoxin CryIB(e)) (cryscaline entomocidal protein) (139 kDa crystal protein).
OS	Bacillus thuringiensis (subsp. kurstaki).				GN Name=cryIBe; Synonyms=15BC2B, cryIB(e);
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				OS Bacillus thuringiensis.
OX	NCBI_TaxId=29339;				OG Plasmid pMYC238.
RN	SEQUENCE FROM N.A.				OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RC	SEQUENCE FROM N.A.				OX NCBI_TaxId=1428;
RA	Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.,				RN SEQUENCE FROM N.A.
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.				RC STRAIN-INNRRL B-15872 / PS158C2;
DR	EMBL; AY570134; AAS93197; -				RC "Bacillus thuringiensis" genes encoding lepidopteran-active toxins."
DR	GO:00050102: P: receptor binding; IEA.				DR Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;
DR	GO:0006552: P: defense response; IEA.				DR FUNCTION: Promotes colloidocal lysis by binding to the midgut
DR	GO:0009405: P: pathogenesis; IEA.				CC epithelial cells of many lepidopteran larvae.
DR	InterPro: IPR001178: Endotoxin.				CC DEVELOPMENTAL STAGE: The crystal protein is produced during
DR	InterPro: IPR005638: endotoxin_C.				CC
DR	InterPro: IPR005639: endotoxin_N.				CC
DR	PFam; PF003944; Endotoxin_C.				CC
DR	PFam; PF00555; Endotoxin_M.				CC
DR	PFam; PF003945; Endotoxin_N.				CC
FT	849				CC
SQ	849 AA;	PCB984957B7CF763	CRC64;		CC
Query Match	29.7%	Score 1013;	DB 2;	Length 849;	
Best Local Similarity	34.9%;	Prod. No. 1.e-57;			
Matches	243;	Conservative 123;	Mismatches 226;	Indels 104;	Gaps 23;

Qy	418 YLGYTKVDFSQYDDQKNETSTQYD-----SKRNNNGIVSAQDSIDQUPPETTDEPLEK 470	Matches 232; Conservative 124; Mismatches 258; Indexes 72; Gaps 17;
Db	416 Y-SWDTNTYFLSSGCVSGISGYTQGIPAVCLQRN-----STDEPLSINPEGDIR 466	Qy 1 MNPNRSEHDTIKVTPNSELQTINHNOYPLADNPNSTBLRNYKEFRLRMEDDSSTEVLJNS 60
Db	-	Db - 1 MNRNPNPEXEYIIDLAPYCGCPSSDDVRYPIASDPAFAQMANYKEYLQTYGDYTGSLNP 60
Qy	471 AYSHOLNAYEBCFLMDRR-----GTLPEFTWTHRSYDFNTIDAEKITOLPVPVKAYA 522	61 TV---KAUGTGTISVVQGILGVVGFAGALTSFYQSFLNTIWP-SDADPKAFMAQE 115
Db	467 NYSHRLSHITQYRFQATQGSPTVANSIPLCTWVTHRVDLNTITANQITQLPLVKAYB 526	61 NLSINPROVLTQGIVNIVERLGFVPGQLYVTFTEILLQMLQWPTNDNAWEAFAEQLE 120
Qy	523 LSSGASITISGPFGTGNLLFLKESSNSTAKFKYTLNSAALLQYVRVRYASTNLRLFV 582	61 VLDKIBIEYAKSKALAEQGLONNDKVDYNALNWKTPLSRSKRSQDRIRELFSQAB 175
Db	527 LSSCATVVGPGFGTGGDV--RRTNTGGFAIRSV-TGLTQYRIRYASTIDFDEV 584	61 ELIDQKISAQVVRNALDDLTGLHDYEEYLAEEWLERNPANGRA---NLVTQRFENLH 176
Qy	583 QNSNNDPLIYVINKTMNKDDLTQTFDIAATTNSNMGFSGDKNEELIGAESFSNEKTYI 642	176 SHFRNSMPSFAV---SKPEVLFPLTYAQAAANTHLILKDAOVFGEEMGYSSEDVAEFPYH 231
Db	585 TRGCTTINNFRERTRMNRSQESRVESTYRVEFTTPFNFTQSODIIRTTSIQLSGNGEVYL 644	177 TAFVTRMPSFGTCPGQSORDAVALLTYYAQAANHLILKDAETYGARGLQQCQINLYFN 236
Qy	643 D 643	Qy 232 RQLKTQYTQDHCYCNWNNGLNRGSTYDANVKENFRREMTLTDLIVLFPFYDTRL 291
Db	645 D 645	Db 237 AQOFRTRAYNHCVETNQGLEYDGRNTESWINYHFRREMTLMAMPLVLPFPYNYRQ 296
<hr/>		
RESULT 39		
C9A_BACTERIA	STANDARD;	TPUSIENS-IRKPHL 334
ID C92N19;	PRT; 1150 AA.	Qy 292 YSKGVKTPBLTRDIFTDPFLSLNTLQEVQP-----TPUSIENS-IRKPHL 334
AC Q92N19;		Db 297 YPNGANPQITRELYTDPIV-----YNPANGICRRCRGWNNPYNTFSELENAPIRPHL 349
DT 16-OCT-2001 (Rel. 40, Created)		Qy 335 FDYLGQIBFHTRIQLQGYFGKDSFNYWSGNVYETRPSIGSSKTITSQYGDKSSTEPVQKL 394
DT 16-OCT-2001 (Rel. 40, Last sequence update)		Db 350 FERLNRLTISRNRYTAPPTNSFLDWSHTLQSQHA--NNPPTYETSYQQTTSNTRLPNT 407
DT 05-JUL-2004 (Rel. 44, Last annotation update)		Qy 395 FDGOKVYRTIANTDVAAMPNGKTYLQGYTKVDFSQYDOKNETSTQTYDSKRNNNGHVSQD 454
DE Pesticidal crystal protein cry9ca (Insecticidal delta-endotoxin CryIXE(a)) (Crystaline entomocidal protoxin) (130 kDa crystal protein)		Db 408 TNGARA-----IDSRAFNFGNFIYANLYGV-----SSLNINFPTGMSBEITNANTCQD 455
DE Name=cry9Ea; Synonyms=cryIXE(a);		Qy 455 SIDQOLPPETDE_PLEXKASHOLNAYAECFLMDRR-----GTIPFFTWTHRSVDFPNT 506
OS Bacteria: Firmicutes; Bacillales; Bacilliaceae; Bacillus.		Db 456 L-----TTTEELPLENNFNFLSHVFLRNFNTTOGGPLATLGFPVTVWTRBDVDFNT 509
OX NCBI_TaxID=1433;		Qy 507 IDABKITOLPVVKAIALSGASLIEPGFTGENLFLIKESSNSTAKFKVTLNSAALLORY 566
RN		Db 510 ITADRTTOLPVWKAISEGGTTVKGPFQFTGGDIL-RRTDGGAVGTRANVN-APLTOQY 567
RP SEQUENCE FROM N.A.		Qy 567 RYRIRYASTTN--LRALFYQNSNNDFLYIYKUMNKKUDDLTYOTFDLATTNSMGSGDK 624
RA Midoh N., Oyama K.;		CC 568 RYRIRYASTTN--LRALFYQNSNNDFLYIYKUMNKKUDDLTYOTFDLATTNSMGSGDK 624
RT Bacillus thuringiensis cry gene for insecticidal crystal protein.";		Db DT 05-JUL-2004 (TREMBLre1. 27, Last annotation update)
RL Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.		DE Crystal endotoxin Cry9Ea.
CC -I- FUNCTION: Promotes colicidomotic lysis by binding to the midgut epithelial cells of insects.		GN Name=cry9Ea;
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.		OS Bacillus thuringiensis.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.		NCBI_TaxID=1428;
CC -I- SIMILARITY: Belongs to the delta endotoxin family.		RN [1] SEQUENCE FROM N.A.
<hr/>		
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RESULTS 40	
CC EMBL: AB011496; BAA34908.1; -	Q71RP4	PRELIMINARY; PRT; 1150 AA.
CC InterPro: IPR001178; Endotoxin.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC InterPro: IPR005638; endotoxin_C.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC InterPro: IPR005639; endotoxin_N.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC InterPro: IPR005640; endotoxin_F.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC InterPro: IPR005641; Endotoxin_C.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC InterPro: IPR005642; Gal_bind_Like.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC InterPro: IPR005643; Endotoxin_M.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC InterPro: IPR005644; Endotoxin_M.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC InterPro: IPR005645; Endotoxin_N.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC Sporulation_Toxin.	ID Q71RP4	AC Q71RP4; PRELIMINARY; PRT; 1150 AA.
CC SEQUENCE 1150 AA; 129895 MW; 7D6AB93D6DC97EB CRC64;	DR GO; GO:0005102; F:receptor binding; IEA.	
DR HSSP; P07130; 1D1C.	DR GO; GO:0006899; Galactosidase; IEA.	
DR InterPro: IPR001178; Endotoxin.	DR GO; GO:0009405; P:defense response; IEA.	
DR InterPro: IPR005638; endotoxin_C.	DR GO; GO:0009405; P:pathogenesis; IEA.	
DR InterPro: IPR005639; endotoxin_N.	DR InterPro: IPR01178; Endotoxin.	
DR InterPro: IPR005640; endotoxin_F.		
DR InterPro: IPR005641; Endotoxin_C.		
DR InterPro: IPR005642; Gal_bind_Like.		
DR InterPro: IPR005643; Endotoxin_M.		
DR InterPro: IPR005644; Endotoxin_M.		
DR InterPro: IPR005645; Endotoxin_N.		
KW Sporulation_Toxin.		
CC SEQUENCE 1150 AA; 129895 MW; 7D6AB93D6DC97EB CRC64;		
Query Match Score 995; DB 1; Length 1150;		
Best Local Similarity 33.8%; Pred. No. 3.le-56;		

DR	InterPro; IPR005638; endotoxin C.	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DR	InterPro; IPR005639; endotoxin N.	NCBI TaxID=29337;
DR	InterPro; IPR00879; Gal_bind_Like.	OX [1] _ SEQUENCE FROM N.A., AND PARTIAL SEQUENCE .
DR	Pfam; PF00344; Endotoxin_C; 1.	RN STRAIN=YCPM_B-1166;
DR	Pfam; PF00555; Endotoxin_M; 1.	RC MEDLINE=99330166; PubMed=10403372; DOI=10.1016/S0014-5793(99)00650-X;
DR	Pfam; PF00345; Endotoxin_N; 1.	RA Wojciechowska J.A.; Lewitin E.; Revina L.P.; Zalunin I.A.,
SQ	SEQUENCE 1150 AA; 129895 MW; 7D6AB93D6EDC97EB CRC64;	RA Chestukhina G.G.;
Query Match	29.2%; Score 995; DB 2; Length 1150;	"Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus thuringiensis sp. <i>finitimus</i> .";
Best Local Similarity	33.8%; Pred. No. 3.1e-56;	RL FEBS Lett. 453:46-48 (1999).
Matches	232; Conservative 124; Mismatches 258; Indels 72; Gaps 17;	CC -!- FUNCTION: Promotes colloidiosmotic lysis by binding to the midgut epithelial cells of insects.
Qy	1 MNPNRSEHDITKTVTPNSELQINHNOYPLADNPNSTLEENYKEFRMTDSSTEVLDS 60	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
Db	1 MNPNRNEYEIIDAYPGCPSPDDDVYPLASDPNPAFQNYKEIQLTYDYCSSLIN 60	-!- SIMILARITY: Toxic segment of the protein is located in the N-terminus.
Qy	61 TV---KDAVGTGISTYVGQTLGVGVGYPPAGALTSPYQOSFLNTIWPSDADWKAQAE 115	-!- SIMILARITY: Belongs to the delta endotoxin family.
Db	61 NLSINPRDVLQZGINTVGRQFLGQVTFPLASPGQVTFPLNQLWPINDNAWEAMQAIE 120	CC
Qy	116 VLIQKILBEYAKSKAALELQQLQNNEDYDYLNSMKTPISLRSKRSQPIRELFSQE 175	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).
Db	121 ELIDQKLISAVYRNALDDLTGLHDYEEYLAEEWLERNGARA---NLVTQRFENLH 176	CC
Qy	176 SHFRNSMPFAV---SKFEVLFPLPYAQAAANTHLLKDQVFGGEWGSSEDVAEPFH 231	CC
Db	177 TAFVTRMPSEFTGPGSQRDAAVIALITYQAQANHLLKDIAEYCARWGJLQQGQNLYN 236	CC
Qy	232 ROLKLTOQYTDDHCVNYYNVNGLRLGSTYDAWKVNFRERENTLTVLDLIVLFPYDIDL 291	CC
Db	237 AQQERTRITYNHCVETNVRGLEDVRGNTNTSLNTHFRERENTLWAMDLVALFPVNVRQ 296	DR EMBL AF122897; AAC25075.1; .
Qy	292 YSKGVVTELLTDIFLTDPFESLNTLQEQGP-----TFLSLENS-TRKPHU 334	DR HSSP_P07130; 1.DLC.
Db	297 YPNGANFQLTRIYTDIV-----YNPANQGICRRGNGNPNTSELENAFRTRPHL 349	DR InterPro; IPR001178; Endotoxin.
Qy	335 FDYQGTEFHTRLQPGYFGKDSFNTYSGNTYTRPSIGSKTTSPYGDKSTEPVQKLS 394	DR InterPro; IPR005639; Endotoxin_N.
Db	350 FERLNLTISRNRYTAPTTNSFLDVSQHTLQSQHA---NNPTTYETSYQQTTSNTRLNT 407	DR InterPro; IPR008979; Gal_bind_Like.
Qy	395 FDGQKVYRTIANTDVAAPNGKRYLVATYKDFQSYDQDNQNETSTQYDSDRNGHVAQD 454	DR Pfam; PF01944; Endotoxin_C; 1.
Db	408 TNGARA---IDSRRARFGENLYANLYGV-----SSLMNPTGMSETNTNAANTCRQD 455	DR Pfam; PF03055; Endotoxin_M; 1.
Qy	455 SIDQLPPTDE-PLEKAYSHOLNAYAECFLMDQRR-----GTPFFTWHSYDFENT 506	DR Pfam; PF03945; Endotoxin_N; 1.
Db	456 L-----TTTEELPLENNNFNLSHYTFLLRNTTQGPLATUFGFTVWTFDFTNT 509	KW Direct protein sequencing; Sporulation; Toxin.
Qy	507 IDAEKITOLPVVKAYALSSGASIIIEGBGFTGGNLFLIKESSNSIAFKVTLNSAALLQY 566	DR SEQUENCE 1163 AA; 131284 MW; 7B5DDEB51341908 CRC64;
Db	510 ITADRTOLPVWKAETGGTGFTVKGFTGDFIL-RRTDGAVGTIRAYN-APITQOY 567	CC
Qy	567 RVIRYASTN--LRLPVONSNDFLVYINKTMNKDDLYQTDFIATNTSMGFSGDK 624	Qy 1 MNPNRSEHDITKTVTPNSELQINHNOYPLADNPNST--BEL-NYKEPLRMTEDESSTE 55
Db	568 RIRLYASTSPEVNLVFNNSAAGFT--LFSMTAQONGSLTYESENTLEVTHTIREQSQD 624	Qy 1 MNPNNRSEHDITKTVTPNSELQINHNOYPLADNPNST--BEL-NYKEPLRMTEDESSTE 55
Qy	625 NELIGAESFVSNEKYIYDKEFIPV 650	Qy 115 EVLIDKKEIYAKSKAALELQGLQNNEFDYNAIANSKKTPSLSLRSKRS --QDRIREL 171
Db	625 TTURLNIFPS1SQQEVVTDKUBIVP1 650	Db 118 EALIDKKSIDAVRNKAISEQGLVNNTLYTEALEEW----LENKENPAVRDVLQRW 171
Qy	RESULT 41	Qy 172 SQAEHFRSNPSFASVSKFEVFLPLPYAQAAQANTHLLKDIAEYCARWGJLQQGQNLYN 231
DB	CQAA BACTF STANDARD; PRT; 1163 AA.	Db 172 RILDGFEOQMPSFAVKGFEVLLVVYTQANLHLLSLRDAYIYGAEWGLTPTNIDQNH 231
AC	QX5597; 16-OCT-2001 (Rel. 40, Created)	Qy 232 RQLKUTQYTDHCVNYYNVNGLRLGSTYDAWKVNFREREMTLDLIVLFPYDIDL 291
DT	16-OCT-2001 (Rel. 40, Last sequence update)	Db 232 RLLRHSAEYDHCVNYYNVNGLRLGSTYDAWKVNFREREMTLDLIVLFPYDIDL 291
DT	16-OCT-2004 (Rel. 44, Last annotation update)	Qy 292 YSKGVVTELTDIFLTDPFESLNTLQEQGP-----TFLSLENS-TRKPHU 339
DT	05-JUL-2004 (Rel. 44, Last annotation update)	Db 292 YP1PTNQFLTREVTYIGKGRNDSDHWSAN---APSFSNLESTLRTPHVDYIK 346
DE	Pesticidal crystal protein cry26Aa (Insecticidal delta-endotoxin	Qy 340 GIE--PHTRLQGPYKDFDSFNYWSGNVYTRPSIGSSKKTTSPPVQKLSFDG 397
DE	CRYXXVIA(a) (Crystalline entomocidal protoxin) (131 kDa crystal	Db 347 KLK1F1PATDVYGTIGRS-GKWHGHIITSATSANTETRN--YGTIVNHDSELNFEG 401
GN	Name=cry26Aa; Synonyms=cry26Aa1, cryXXVIA(a);	OS 398 QKVRYRANTDVAWNG-----KVLYGVTKDFQSYYDDONNETSTQTYDSKR-- 445
OS	Bacillus thuringiensis (subsp. <i>finitimus</i>).	

Db	402	KNIYKII-----GSLPQGPBPYQIGXVTPYFITRAVNFTVSSSK--TSEVKYSSKKR	453	Db	139	RA---NIVLQRFBILHALFVSSNIPSFGSGPGSDFRQAGLIVVYAAQAANTHLULLADAER	194
Qy	446	-NNGHVSAQD--SIDQLPBTTEPLEKAYSHQNLNYAACFLQMDDR--GTPPFITWTH	498	Qy	215	FGBEWGYSSBBDVAFPHQKL-TQOYTDHCVNVNGLRSSTYDAWKENFRFREM	273
Db	454	YYSEGLPPEEQVFSTEQQPNNSIAEPHAYSHRLCHVTETISVSNNGNKYSKDLPLFSWTH	513	Db	195	YGAWRGLRQEQQNLYFENLQTRTRDYNTHCVNAYNNGLAGLRTGTSAESWLKYHQFRREA	254
Qy	499	RSVDPFNTDAEKQTQLPVKPKAYALUSGSASIIEPGFTGQNLLPKESSNSIAKEFKVTLN	558	Qy	274	TLTVDLTLVLPFPYDILRYSKGVTKELTIDTFDP-----IFSINTLQEYGP	320
Db	514	SSVDPDNYVPTKTTOLPATKGY---NYSIVKEPGFIGDDI-GKNNQIQLGKYKVNV	567	Db	255	TLMADDLIALFPYNTTRYPIANVQLREVYDPLGPSEEESSLPEIRCLRNQETSAM	314
Qy	559	SAALLQRYVRVIRYIASTTNLRLFYQNSNDFLVYIINKTMNKDDDLTYCOTFLATTSNM	618	Qy	321	TFLSIENS-IRKPHLFDFYLOGIBFHTRLQPGYFGKDSFNYWSGNVYETRPSIGSSKTITS	379
Db	568	DVS--QKYRPRVRIATEBEGLKGIDGTWNLQYKTKAPGDPFLTKAFDYLSSLFSTWV	625	Db	315	TFSNLENATISSPLFDTINNLMTYGSVSHLTLNQLEGWIGHSVTSSLASGPTTVLR	374
Qy	619	GFSGDKNELIJIGAEFFVSNB--KIVYDKEFIPVQ	651	Qy	380	PFYGDKSSTEPVQKLSPFGQKVR-TIANTDVAAPNGKVLGYTUVDEQYDDQKNETS	437
Db	626	KFNNASTTI---ELFLQNRKTSGTFLYLAGIEIIIPVK	657	Db	375	RNYG-STTSIVNYESFENDRDVYQINTSRSHGL-GFQNAPLF-GTRAQF-----YP	422
Qy	627	RESULT 42		Qy	438	TQYDSDERNGHVSAAQ--DSIDOLPPTTDEPKAYSHQNLYAECFL-----MODR	487
Q45745		PRELIMINARY;	PRT;	Db	423	GTYSTVQRNALTCEQNYNSIDEPLSDNEPISRSYKSHRLSHITSYLRHVLTDGINY	482
ID	Q45745;			Qy	488	RGTIPFFWTMHSYDFNTTIDAKitOLPVKAYALSSGASITLEPGFETGGNLLFLKLESS	547
AC	Q45745;			Db	483	SGLNPTWTHRDVDTLNNTADRTQLPLVSKFPIAGTVVRGPGFTGGDIL-RRTCV	541
DT	01-NOV-1996	(TREMBLrel. 01, Created)		Qy	548	NSTAKEKUTLNSAALQRYVRVRYAYSTNLRLFVQNSNNDFLVYIINKTMNKDDDLTYQ	607
DT	01-NOV-1996	(TREMBLrel. 01, Last annotation update)		Db	542	GTRGTRIVR-TTAPLTOYRVRFRFATNLFIGRVDRQVNYXFDFCRTMNGDELRYE	600
DT	01-NAR-2004	(TREMBLrel. 26, Last annotation update)		Qy	608	TFDIATTNSNMGSGDNELITGAESFSVNEK1YIDKLFIPV	650
DE	Delta-endotoxin (Fragment).			Db	601	SPATREFTTDNFNFRQPOBLISVFAANAFSAGQEVYPDRIEIIPV	643
GN	Name=cryIX gene;			Qy	628	RESULT 43	
OS	Bacillus thuringiensis.			CLCA_BACTE			
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				AC	P05518; P10327; Q03742; Q45725;		
NCBI_TaxID=1428;				ID	CICA_BACTE	STANDARD:	PRT;
RN	SEQUENCE FROM N.A.			DT	01-NOV-1988 (Rel. 09, Created)		
RA	Shavelev A.B., Svirinsky M.A., Karasik A.I., Kogan Y.N.,			DT	30-MAY-2000 (Rel. 39, Last sequence update)		
RA	Chestukhina G.G., Stepanov V.M.,			DT	05-JUL-2004 (Rel. 44, Last annotation update)		
RT	"Primary structure of the cryIX*-the novel Delta-endotoxin-related			DE	Pepticidial crystal protein cryICa (Insecticidal delta-endotoxin)		
RT	gene from Bacillus thuringiensis spp. <i>Galleriae</i> ;"			DE	CryIC(a) (Crystalline entomocidal protein) (134 kDa crystal protein).		
RT	RT			GN	Name=cryICa; Synonyms=cryIC, cryIC(a);		
RT	RT			OS	Bacillus thuringiensis (subsp. <i>aizawai</i>), and		
RT	RT			OS	Bacillus thuringiensis (subsp. <i>entomocidus</i>), and		
RT	RT			OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
RT	RT			NCBI_TaxID=1436,	1433;		
RN	SEQUENCE FROM N.A.			RN	[1]		
RP	SPECIES=B.t. entomocidus; STRAIN=50.5;			RP	SEQUENCE FROM N.A.		
RP	SPECIES=B.t. aizawai; STRAIN=NRRRL B-18484 / PS811;			RC	SPECIES=B.t. aizawai; Published=339402;		
RP	SPECIES=B.t. entomocidus; STRAIN=50.5;			RX	Medline=89289380; PubMed=2348060;		
RP	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RA	Hone G., van der Salm T.P.M., Visser B.;		
RP	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RT	"Nucleotide sequence of crystal protein gene isolated from <i>B. thuringiensis</i> subspecies <i>entomocidus</i> 60.5 coding for a toxin highly active against Spodoptera species.";		
RP	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RL	Nucleic Acids Res. 16:6240-6240(1988).		
RP	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RN	[2]		
RP	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RP	SEQUENCE FROM N.A.		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RC	Specie=B.t. aizawai; STRAIN=NRRRL B-18484 / PS811;		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RX	Specie=B.t. aizawai; Published=339402;		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RA	Medline=89289380; PubMed=2348060;		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RT	"Bacillus thuringiensis isolate active against lepidopteran pests, and genes encoding novel lepidopteran-active toxins.";		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RL	Patent number US246852, 21-SP-1993.		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RN	SEQUENCE OF 1-823 FROM N.A.		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RC	Specie=B.t. aizawai; STRAIN=7-29;		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RX	Medline=89313627; PubMed=2348060;		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RA	Sánchez V., Lerechus D., Menou M., Chauaux J., Guo S., Lecadet M.-M.,		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RT	"Nucleotide sequence and analysis of the N-terminal coding region of the Spodoptera-active delta-endotoxin gene of <i>Bacillus thuringiensis</i>		
RC	Specie=B.t. aizawai; PAYNE J.M., Sick A.J., Payne J.M., Sick A.J.,			RT	the Spodoptera-active delta-endotoxin gene of <i>Bacillus thuringiensis</i>		

DE	CryIA type crystal protein (Fragment).	01-JAN-1988 (Rel. 06, Last sequence update)
OS	Bacillus thuringiensis (subsp. <i>kenyae</i>)	05-JUL-2004 (Rel. 44, Last annotation update)
OC	Bacteriae; Bacillales; Bacillaceae; Bacillus.	DE Pesticidal crystal protein cry1Ab (insecticidal delta-endotoxin).
NCBI_TAXID	33930;	DE Cry1A(b) (crystalline entomocidal protoxin) (130 kDa crystal protein).
[1]	SEQUENCE FROM N.A.	GN Name=cry1Ab; Synonyms=bt2, cry-1-2, cryIA(b), cryIA(bt), cryICl;
RC	STRAIN=N33;	OS Bacillus thuringiensis (subsp. <i>kurstaki</i>)
RA	Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.; Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	OS Bacillus thuringiensis (subsp. <i>berliner</i>)
DR	EMBL: AY570735; AAQ93798; 1.	OS Bacillus thuringiensis (subsp. <i>aizawai</i>).
DR	GO: GO:0005102; F:receptor binding; IEA.	Plasmid.
DR	GO: GO:0009405; P:defense response; IEA.	OG Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DR	InterPro: IPR001178; Endotoxin.	OC
DR	InterPro: IPR005638; endotoxin C.	OX
DR	InterPro: IPR005639; endotoxin N.	RN [1] — TaxID=29339, 1434, 1433;
DR	InterPro: IPR008979; Gal bind Like.	RP SPECIES=B.t. <i>kurstaki</i> ; STRAIN=HD-1;
DR	Pfam; PF00344; Endotoxin_C; 1.	RC MEDLINE=87163505; PubMed=3557124; DOI=10.1016/0378-1119(86)90357-4;
DR	Pfam; PF00055; Endotoxin_M; 1.	RX Geiser M., Schweiter S., Grimm C.; "Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from <i>Bacillus thuringiensis</i> var. <i>kurstaki</i> HD-1 DNA." RT
DR	Pfam; PF003945; Endotoxin_N; 1.	RT Genes 48:109-118 (1986). RT
FT	NON_TER 793 793 MW: 89492 MW: 04FD0E79788E53DB CRC64;	RL Gene 48:109-118 (1986). RN
SQ	SEQUENCE 793 AA; 89492 MW;	[2] RN
QY	Query Match 26.7%; Score 909; DB 2; Length 793;	RP SEQUENCE FROM N.A.
Db	Best Local Similarity 34.8%; Pred. No. 7.9e-51;	RC SPECIES=B.t. <i>kurstaki</i> ; STRAIN=HD-1;
Matches	Matches 208; Conservative 114; Mismatches 210; Indels 66; Gaps 19;	RX Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.; RA "Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from <i>Bacillus thuringiensis</i> var. <i>kurstaki</i> HD-1 DNA." RT
QY	82 VPFGAGLTSFYOSFLNTIW---PSDADPKAFMAQVEVLDKCKTEBYANGSKALALQGL 137	RA Hefford M.A., Brousseau R., Prefontaine G., Hanna Z., Condie J.A., AgriC. Biol. Chem. 51:455-463 (1987). RL
Db	44 VPGAG---FVGLVDIINGIGFQPSQ---WDAFLVQEQLINQRIEEFARNOAISRLEGI 96	RN [3] —
QY	138 QNNFEDVYNALNSWKTKPLSLRSKRSQRDLFELSQAESHRNNSMPSFAYSFKFEVLFLPF 197	RP SEQUENCE FROM N.A.
Db	97 SNUYQIVAESFRWAEDPTN-PALRVMRITQ--FNDMNSALTATTAILFAVONYQFPLSV 153	RC SPECIES=B.t. <i>kurstaki</i> ; STRAIN=NRD-12;
QY	198 YAQAANTHLLKKDAQVFGEEGNGSSDVAEFYHROLKLTOQYTDHCVNNTVNGLNLRG 257	RX MEDLINE=86223796; PubMed=301746; RA Thorne L., Gardiner F., Thompson T., Decker D., Zounes M., Wild M., Waller A.M., Pollock T.J.; RA "Sequence of a lepidopteran toxin gene of <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> NRD-12." RT
Db	154 YYQAANTHLLSVLRDVSVFQRMGFDDATINSRNYNDLTRLIGNYTDIAVRWNTGLERWG 213	RT J. Biotechnol. 6:307-322 (1987). RL
QY	258 STYDAWKPNPFRREMTLVLIDLVLPPFYDILRYSKGKVTELTRDFTDPFLSNTLQ 317	RN [4] RN
Db	214 PDSRDWIRYNOFPRELITLVLDVSLSPNPDYSDRTYPIRTVSQLTRELYTNPV---LED 268	RP SEQUENCE FROM N.A.
QY	318 YGPTE---LSTENSIRKPHLPYLOGTEFHTRLQPGYFKGDTSFNTWGNVETRPSIGS 373	RC SPECIES=B.t. <i>kurstaki</i> ; STRAIN=HD-1;
Db	269 FNGSFRGSAQGEQSIRSPLHDLINSITYDARGYY----YWSGHQIMASPVGF 322	RX MEDLINE=8630052; PubMed=3743328; RA Silva-Wernick J.O., De-Souza M.T., Dias J.M.C.S., Ribeiro B.M.; RA "Characterization of <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> strain S93 effective against the Fall armyworm, <i>Spodoptera frugiperda</i> and cloning of a cry1Ab gene." RT
QY	374 SKITPSFYGDK-STEPVQKLSFD-GKRYVRTANTDVAWPNKGKYTLGTVDFSYQYDD 431	RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
Db	323 3PBPFTPLGYTMGNAAPQORIVAAQLGQEVYRTLSST---FVRSPFNIGNNQQLSVLDG 378	RN [5] RN
QY	432 QRNETSQT----YDSKRNGNHVSAQDSIDOLPPTTDEPLEKAYSHQNYAECFLMQ 485	RP SEQUENCE FROM N.A.
Db	379 TEPAYGTSNLPNSPAVY---RKSCSTV---DSLDRIPONNNVPQRGPSRLSHVSMFRSG 432	RC SPECIES=B.t. <i>berliner</i> ; STRAIN=1715;
QY	486 DRRTI----PSPFTWTHRSVDSFNTIDAEEKTDLTPVVKAYALSSGRSISIEPGFGCGNL 540	RX MEDLINE=87054056; PubMed=3023051; RA Wabicius H., Raymond K.C., Bulla L.A. Jr.; RA "Bacillus thuringiensis" entomocidal protoxin gene sequence and gene product analysis." RT
Db	433 FSNSSVSIRAPMFSWTHSAEFPNLIIPSQQTPLKTNSTLGSCTSVKSPGFTCGDI 492	RT DNA 5:305-314 (1986). RL
QY	541 LFLLKESSNSIAKEPKVTLNSSLQLQYRVRIRASTTNRLFVQ-----NSNNDFLYIY 594	RN [6] RN
Db	493 L-RRTSPGQDISTLRVN-TAPLSQRYRTRIVASTTNLQPHTSIDGRPINQGN-----F 544	RP SEQUENCE FROM N.A.
QY	595 NKTMANKDDDTYQFEDLATNSNMNGFSGCDKNELLIGAEFVNEEKITDKTFIFPVL 652	RC SPECIES=B.t. <i>berliner</i> ; STRAIN=1715;
Db	545 SATMSSGSNLQSGSFRTAGFTDPENFSNGSSVFTLSAHVFNSNEVIDRIEFFVPAEV 602	RX MEDLINE=87054056; PubMed=3023051; RA Hoeft H., de Greve H., Seurinck J., Jansens S., Mahillon J., Ampe C., RA Vandekerckhove J., Vandeebrugge H., van Montagu M., Zabeau M., RA Vaeck M.; RA "Structural and functional analysis of a cloned delta endotoxin of <i>Bacillus thuringiensis</i> Berliner 175." RT
RESULT	47	RT Eur. J. Biochem. 161:273-280 (1986). RN
C1_PBS_BACTK	STANDARD	RN [8] SEQUENCE FROM N.A.
ID	C1AB_BACTK	RT
AC	P06578; P06577; P09663; P09666; P21257;	RT
DT	01-JAN-1988 (Rel. 06, Created)	RP

RC	SPECIES=B.t. aizawai; STRAIN=HD-133;	L -> P (in Ref. 4). LSH -> CLAY (in Ref. 4).			
RT	"Complete nucleotide sequence and identification of a putative promoter region for the expression in Escherichia coli of the cryIA(b) gene from Bacillus thuringiensis var. aizawai HD133.";	R -> Y (in Ref. 4). I -> V (in Ref. 4). A -> P (in Ref. 10). MFSWIHR -> NDSSwtrIC (in Ref. 4).			
RL	Proc. Natl. Sci. Counc. Repub. China, B, Life Sci. 17:7-14 (1993).	E -> N (in Ref. 3). NNI -> GDV (in Ref. 4). SPNLGSGT -> LOSWtWN (in Ref. 4).			
RN	SEQUENCE FROM N.A.	P -> L (in Ref. 4). RTSP -> EELT (in Ref. 4).			
RP	SEQUENCE FROM N.A.	P -> L (in Ref. 4). K -> NG (in Ref. 3). S -> N (in Ref. 4). D -> H (in Ref. 3). P -> I (in Ref. 10). T -> L (in Ref. 10). TV -> HL (in Ref. 3). K -> E (in Ref. 3). KR -> NG (in Ref. 3). S -> N (in Ref. 4). D -> H (in Ref. 7). P -> L (in Ref. 7 and 10). P -> R (in Ref. 7 and 10). P -> R (in Ref. 3). P -> I (in Ref. 3). Q -> H (in Ref. 9). E -> T (in Ref. 3). C -> F (in Ref. 9). B -> G (in Ref. 3).			
RC	SPECIES=B.t. aizawai; STRAIN=IC1;	FT	CONFLICT 410 FT	410 430 437 437 447 447 450 452 461 463 479 492 501 537 542 545 568 569 492 505 537 542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	410 432 437 437 447 447 450 452 461 463 479 492 501 537 542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 492 FT	492 505 537 542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	492 505 537 542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 501 FT	501 537 542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	501 537 542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SPECIES=B.t. aizawai; STRAIN=IC1;	FT	CONFLICT 537 FT	537 542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	537 542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 542 FT	542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	542 545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 545 FT	545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	545 568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 568 FT	568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	568 569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 569 FT	569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	569 665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 665 FT	665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	665 675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 675 FT	675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	675 703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 703 FT	703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	703 712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 712 FT	712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	712 731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 731 FT	731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;	731 785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 785 FT	785 836 978 1016 1036 1060 1155 AA; 130623 MW;	785 836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 836 FT	836 978 1016 1036 1060 1155 AA; 130623 MW;	836 978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 978 FT	978 1016 1036 1060 1155 AA; 130623 MW;	978 1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 1016 FT	1016 1036 1060 1155 AA; 130623 MW;	1016 1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 1036 FT	1036 1060 1155 AA; 130623 MW;	1036 1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 1060 FT	1060 1155 AA; 130623 MW;	1060 1155 AA; 130623 MW;
RC	SEQUENCE FROM N.A.	FT	CONFLICT 1155 AA; 130623 MW;	1155 AA; 130623 MW;	1155 AA; 130623 MW;
CC	Query Match	Qy	26.4%; Score 899.5; DB 1; Length 1155;		
CC	Best Local Similarity	Qy	33.3%; Pred. No. 5.6e-50;		
CC	Matches	Qy	220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;		
CC	CC	Qy	31 DNPNSTLFEELNKYKEFLRMEKTYKTDVLDNSTVYKTDVATGVTISUVG-----QILGVGVPF 84		
CC	CC	Db	3 NNPNIN-ECIPY---NCLSNPEVEGLIGERIE---TGYTPDIDSLSLTQLPNSFSEVFPGV 53		
CC	CC	Qy	85 AGALTISFYQSPLNTIW---PSDADPKAFMAQVEVLIDKKLEBEYAKSKALAEQLGLONN 140		
CC	CC	Db	54 AG---FVGLVDIINGIFGFPQSO---WDAFLVQIEQLINQRIEEFARNOAISRLEGLSNL 106		
CC	CC	Qy	141 FEDYVNALNSWKTPLSLRSKRSQRDRLEFLSQAESHRFRNSNMSFAVSKFEBVLFPLPTYAQ 200		
CC	CC	Db	201 AANTHLLJLKDQFGEWGSSEDDVAFYHQKLQTQYTHCWNVYNGLNGLRGSTY 260		
CC	CC	Db	164 AANLHLSSVLRDVSFGWRGFDAAATINSRYNDLTLIGNTYDHAVRYNTGLERVGWDGS 223		
CC	CC	Qy	261 DAWVKFNRERREMTLTIVLVPFPYDIRLYSKGVKTELTDIFTPISLNTLQEYGP 320		
CC	CC	Db	224 RDWYRQNFRRRETTLVLDIVSLFNPYDSRTPIRTVSQLTRBYTNPV----LENFDG 278		
CC	CC	Qy	321 TF---LSIENSTKPHLFEDYLGQIEPFTRLOGYGRDSDPYWGNVETRPSIGSSRT 376		
CC	CC	Db	279 SFPGSAGGIEGSTSRSPHLMIDLINSITIYTDAHGREY----YWWSHOIMASPVFGSGPE 332		
CC	CC	Qy	377 ITSPPYGDK-STEPVQKLSEFD-GQKYRTIANTDVAAWPNGKVY----LGITTKVDFQY 429		
CC	CC	Db	333 FTEPLYGMGNAAQPQRIVAQGQGVTLLSS-----LYRPRPNIGNNQQLSVL 383		
CC	CC	Qy	430 DDQKNETSTQT----YDSKRNNNGHVAQDSIDQLPETTDEPLEKASHQLNAYAECFL 483		
CC	CC	Db	384 DGETFAYGTSSNLPSSAVY--RKGSTV---DSLDEIPQNNNVPRQGFSHRLSHVSMFR 437		
CC	CC	Qy	484 MDRRGTI----PFTFWTHRSVDFNTIDAEKITDLPVRAYALSSASILEGPGFPTGG 538		
CC	CC	Db	438 SGFSNSSVSIIRAPMFMSWIRSAEFPNNIIPSSOITQPLTKSTNLGSCTSVMKPGFTGG 497		
CC	CC	Qy	539 NULLFLKESNSNSTAKFYTLLNSALLOQYVRVRYASTNTNLRFVQ----NSNNDFLAVI 592		
CC	CC	Db	498 DIL-RTRSPGQ1STLRVNI-TAPLSQRYVRVRYASTTNLQFHTS1DGRPINQGN----LKFQGPPPTEKAP (in Ref. 4).		

Qy	593 YINKTMNKDDDTYQTDFLATTNSNMGFSGDKNELLIGAESFSNEKIXYDKEFIPVQL 652	Qy	430 DDQKNETSTQT-----YDSKRNNGGHVSAAQPSIDOLPPETTDEPLERKASHOLNYAECAFCL 483
Db	551 -FSATMSSGSNLQSOSFRTRVGTTPFSNGSVFTISAHVFNNSGNVEVDRIEFVPAEV 609	Db	384 DGTEFAGTSNLPSAVY--RKGTV--DSLDEPPQNINVPFGSFRSLSHSLSMFR 437
RESULT 48			
Q7BE98	PRELIMINARY;		
ID Q7BE98	PRT; 1155 AA.		
AC Q7BE98_			
DT 05-JUL-2004 (TREMBLrel. 27, Created)			
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE Crystal endotoxin CryIAb (Insecticidal protein P).			
GN Name=cryIAb			
OS Bacillus thuringiensis.			
OC Bacteria; Firmicutes; Bacillales; Bacilliaceae; Bacillaceae; Bacillus.			
OX NCBI_TaxID=1428;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=B-Hm-16;			
RA Li C.; Zhang J.; Ji G.; Huang D.;			
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
STRAIN=Btc005;			
RC TAN J., ZHANG J., WANG K., HUANG D.;			
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
EMBL; AF358861; AA013302.1;			
EMBL; AF254440; AA076494.1;			
DR GO; GO:0005102; F: receptor binding; IEA.			
DR GO; GO:0006552; P: defense response; IEA.			
DR InterPro; IPR001178; Endotoxin.			
DR InterPro; IPR001178; endotoxin.			
DR InterPro; IPR005638; endotoxin_C.			
DR InterPro; IPR005639; endotoxin_N.			
DR InterPro; IPR008979; Gal_bind_Like.			
PFam; PF03944; Endotoxin_C; 1.			
DR Pfam; PF03945; Endotoxin_M; 1.			
DR Pfam; PF03945; Endotoxin_N; 1.			
SQ SEQUENCE 1155 AA; 130623 MW; 43461A64C7ACTCAFP CRC64;			
Query Match Score 899.5; DB 2; Length 1155; Best Local Similarity 33.3%; Pred. No. 5.6e-50; Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;			
Qy 31 DNPNSTLEELNKYKEFLRMTEDSSTEVLNDSTVKDAVTGTSVGV----QILGVGVYPF 84	Qy 31 DNPNSTLEELNKYKEFLRMTEDSSTEVLNDSTVKDAVTGTSVGV----QILGVGVYPF 84		
Db 3 NNPNIN-ECIPI---NCLSNPBEVLLGGERIE---TGTPIDISLSLTQFLLSEFVPG 53	Db 3 NNPNIN-ECIPI---NCLSNPBEVLLGGERIE---TGTPIDISLSLTQFLLSEFVPG 53		
Qy 85 AGALTSFYQSFINTIW---PDADEPKWAKFAQVEVLIDKLEEYAKSKALAELQQLNN 140	Qy 85 AGALTSFYQSFINTIW---PDADEPKWAKFAQVEVLIDKLEEYAKSKALAELQQLNN 140		
Db 54 AG---FVLGVDIINGIFGPFSQ--WDAFLVQIEQLINQRIEFPARNQASIRLEGSLNL 106	Db 54 AG---FVLGVDIINGIFGPFSQ--WDAFLVQIEQLINQRIEFPARNQASIRLEGSLNL 106		
Qy 141 FEDYVNALNSWKTKPLSLRSRSQRDRFLRELFSAQESHSFRNMSPSFAVSKFVFLPTYAQ 200	Qy 141 FEDYVNALNSWKTKPLSLRSRSQRDRFLRELFSAQESHSFRNMSPSFAVSKFVFLPTYAQ 200		
Db 1.07 YQIAESFREWEADPTN-PALREMRIO---FNDMNSALTAITPLFAVQNCYPLSVYQ 163	Db 1.07 YQIAESFREWEADPTN-PALREMRIO---FNDMNSALTAITPLFAVQNCYPLSVYQ 163		
Qy 201 AANTHLLIKDQAQVEGLGQFGEWGISSDEDAEFYHRQLKLTQOQTDHCYWNWYNGLNGRSTY 260	Qy 201 AANTHLLIKDQAQVEGLGQFGEWGISSDEDAEFYHRQLKLTQOQTDHCYWNWYNGLNGRSTY 260		
Db 164 AANLHSLSVLRDVSFGQRWGFDAATINSRNDRTRIGNYTDHAYRWNTCLERYWGPDS 223	Db 164 AANLHSLSVLRDVSFGQRWGFDAATINSRNDRTRIGNYTDHAYRWNTCLERYWGPDS 223		
Qy 261 DAWVKENPRREMILTLTLDLWLPFDYFLDIRLYSKGVKTTELDRDTPISLNTLOEYGP 320	Qy 261 DAWVKENPRREMILTLTLDLWLPFDYFLDIRLYSKGVKTTELDRDTPISLNTLOEYGP 320		
Db 224 RDWTRYNQFRRELTLTLDLWLPFDYFLDIRLYSKGVKTTELDRDTPISLNTLOEYGP 278	Db 224 RDWTRYNQFRRELTLTLDLWLPFDYFLDIRLYSKGVKTTELDRDTPISLNTLOEYGP 278		
Qy 321 TP---LSIENSIRKPHLFYDLYQGQFTRHTRLQPGYFGKDSFNYWSGNVYTRPSIGSSKT 376	Qy 321 TP---LSIENSIRKPHLFYDLYQGQFTRHTRLQPGYFGKDSFNYWSGNVYTRPSIGSSKT 376		
Db 279 SFRGSAQIGESIRSIRSPHLMDLINSITYTDHARGEY----YWSGHQIMASPVGFSGP 332	Db 279 SFRGSAQIGESIRSIRSPHLMDLINSITYTDHARGEY----YWSGHQIMASPVGFSGP 332		
Qy 377 ITSPFYGDK-STEPYOKLSD-FQKYTRTIANTDVAAPNCKVY----LGVTKVDFSQY 429	Qy 377 ITSPFYGDK-STEPYOKLSD-FQKYTRTIANTDVAAPNCKVY----LGVTKVDFSQY 429		
Db 333 FTFPLYGTGMGNAAPOQRIVAQLGQGVYRTLSST-----LYRRPFNINNOOLSVL 383	Db 333 FTFPLYGTGMGNAAPOQRIVAQLGQGVYRTLSST-----LYRRPFNINNOOLSVL 383		
Qy	551 -FSATMSSGSNLQSOSFRTRVGTTPFSNGSVFTISAHVFNNSGNVEVDRIEFVPAEV 609	Qy	551 -FSATMSSGSNLQSOSFRTRVGTTPFSNGSVFTISAHVFNNSGNVEVDRIEFVPAEV 609

Db	279 SFRGSAQGLEGGSIRSPLHMDILNSITIYDAHRGEY-----YWSGHQIMASPVGFSGPE	332	Db	224 RDWIRYNQFRRELTVLTDIVSLFPNYDSRTYPIRTVSOLTREIYTNPV-----LENFDG	278	
Qy	377 ITSPPYGDK-K-STEPVQKLSD-GOKVYRITANTDVAWWNGKVY-----LGVTKVDFSY 429		Qy	321 TF-----LSIENSIRKPHLFDYLOGIEFHTRLQPGYFGKDSFNTYMSGNYVETRPSIGSSKT	376	
Db	333 FTFFPLYGMCGNAAPQRIVAQOLGGCVYRPLSST-----LYRPPFNGINNQQLSVL	383	Db	279 SFRGSAQGLEGGSIRSPLHMDILNSITIYDAHRGEY-----YWSGHQIMASPVGFSGPE	332	
Qy	430 DDQKNETST-----YDSKRANGHVSQAQSDTQPLPPTTDEPLEKAYSHOLNYAECFL	483	Qy	377 ITSPFYGDK-STEPVQKLSD-GOKVYRTIANTDVAAWPNNGKVY-----LGVTKVDFSY	429	
Db	384 DGTEPAYGTSNNLPBAVY---RKSCTV---DSLDRPPONNNVPROQGSHRLSHVSMFR	437	Db	333 FTFFLYGMGNAAFQRIVAQOLGGCVYRPLSST-----LYRPPFNGINNQQLSVL	383	
Qy	484 MQDRRGTI----PFPTWTHRSVDFFNTIDAEEKITQPLPVKAVALSSGSSIIEGPGFTGG	538	Qy	430 DDQKNETSTQ-----YDSKRANGHVSQAQSDTQPLPPTTDEPLEKAYSHOLNYAECFL	483	
Db	438 SGFSNNSVSVTIRAPMFSWTHRSALFENNLIPSSQITQPLTKSTNLGSGTSVVKGPGETGG	497	Db	384 DGTEFAYGTSSNULPSAVY---RISGTV---DSLDIPIPPONNNVPROQGSHRLSHVSMFR	437	
Qy	539 NLLFLKESNSNIAKEPKVTNSAALLQRYVRVIRYASTTNLRLFVQ-----NSRNNDFLV	592	Qy	484 MQDRGTI----PFPTWTHRSVDFFNTIDAEEKITQPLPVKAVALSSGASIIEGPGFTGG	538	
Db	498 DIL-RRTSDPQQISTLRVN1-TAPLSQRYVRVIRYASTTNLQFHTSIDGRPINGQN-----	550	Db	438 SGFSNNSVSIIGAPMFSWIHSABFNNTIPSSQTQPLTKSTNLGSGTSVVKGPGETGG	497	
Qy	593 YINKTMNKDDDLTYQTEDLATTNSMGFGDKNEELIGAESFSVNEKLYIDKLEFIPVQL	652	Qy	539 NLLFLKESNSNIAKFKYTLNSAALLQRYVRVIRYASTTNLRLFVQ-----NSRNNDFLV	592	
Db	551 -FSATMSSSNLQSGSSNLFQSGSFRTVGFITPPENFNGSSVFTLSAHVFNSGNEYTIDREFVPAEV	609	Db	498 DIL-RRTSPFGQISSLRVNI-TAPLSQRVRYATSNLQFHTSIDGRPINGQN-----	550	
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RESULT 50			Qy	593 YINKTMNKDDDLTYQTEDLATTNSMGFGDKNEELIGAESFSVNEKLYIDKLEFIPVQL	652	
ID Q6GUAT	PRELIMINARY;	PRT; 1156 AA.	Db	551 -FSATMSSSNLQSGSSNLFQSGSFRTVGFITPPENFNGSSVFTLSAHVFNSGNEYTIDREFVPAEV	609	
AC Q6GUAT_			Search completed: February 14, 2005, 15:23:13 Job time : 187 secs			
DT 05-JUL-2004 (TREMBurel, 27, Created)						
DT 05-JUL-2004 (TREMBurel, 27, Last sequence update)						
DT 05-JUL-2004 (TREMBurel, 27, Last annotation update)						
OS Parapsopla crystal Protein.						
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.						
OX NCBI_TaxID=1428;						
RN	SEQUENCE FROM N.A.					
RA Huang Z., Guan C., Guan X.;						
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.						
DR EMBL; A164616; ANT46415.1;						
DR GO:0005102; F receptor binding; IBA.						
DR GO:0006952; P defense response; IBA.						
DR GO:0009405; P pathogenesis; IBA.						
DR InterPro: IPR001178; Endotoxin.						
DR InterPro: IPR005638; endotoxin_C.						
DR InterPro: IPR005639; endotoxin_N.						
DR InterPro: IPR0008919; Gal_bird_Like.						
DR Pfam; PF03944; Endotoxin_C.						
DR Pfam; PF00555; Endotoxin_M.						
DR Pfam; PF03945; Endotoxin_N.						
SQ SEQUENCE 1156 AA; MW; 1759B23E3DAA4A09 CRC64;						
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Query Match 26.4%; Score 898.5; DB 2; Length 1156;						
Best Local Similarity 33.3%; Pred. No. 6.5e-50;						
Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;						
Qy 3 DNPNSTLEFLNKKFELRMTEDSSTEVLDSNTVKAQV-----QILGVVGVPF 84						
Db 85 AGALTFSYFSFLNTIW---PSDADPWFKAQV-----QVLIKKIBEAKSKALABQGLQNN 140						
Qy 54 AG---FVIGLVDIWIQGTSQ --WDFPLVQEQLINQRIEFARNQAIISLEGISNL 106						
Qy 141 FEDVNALNSWKCPPLSLRSKRSQDRINELFQSASHERNSMSFAVSKFEVFLPLTAQ 200						
Db 107 YQTYAESPWEADPTN-PALRFEMRQI-FNDMNSALTALEFAYVQYQPLLSYYVQ 163						
Qy 201 AANTHLLIKDQAQVGEENGYSSEDDAEYTHRQLKLTOQYTDHCWNWNVGLRLRSSTY 260						
Db 164 AANLHLPVLRDVSVFGQRNGFDAATINSRNYNDLTRLIGNYTDIAVRNTNGLERVWGPDS 223						
Qy 261 DAIVVKFNRPRREMTLTVLPLIVLQPFYDRLYSLRGVKTLETRDIFTDPIFSINTLQYGP 320						

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